

STIC Search Repor Biotech-Chem Library

STIC Database Tracking Number: 98347

To:

Daniel Sullivan

Location: CM1-11E12

Art Unit:

1636

Thursday, July 17, 2003

Case Serial Number: 09/914191

From:

Beverly Shears

Location: Biotech-Chem Library

CM1-1E05

Phone:

308-4994

beverly.shears@uspto.gov

Search Notes

Daniel,

Due to seq. length, unable to search amino acid query. I did, however, search Seq. ID 1 in the AA dBs.

Beverly

Note: Qy his and 1 Seg 0. 99.8% - 100% match



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STIC-Biotech/ChemLib

From: Sent:

Sullivan, Daniel

Tuesday, July 08, 2003 4:18 PM STIC-Biotech/ChemLib

To: Subject:

Search Request 09914191

Please search for the following in the commercial and issued patent databases:

-a nucleic acid comprising SEQ ID NO:1

Also, I have reason to believe that the reverse complement of SEQ ID NO:1 encodes all or a portion of the following amino acid sequence:

MTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQTLKDYLSWRQADCHINNLYNTVFW ALIQQSGLTPVQAQGRLQGTLAADKNEILFSEFNINYNNELPMYRKGTVLIWQKVDEVMTKEIKLPTE MEGKKMAVTRTRTKPVPLHCDIIGDAFWKEHPEILDEDS

would it be possible to search this amino acid sequence against the commercial and issued patent databases as well?

Thanks, Dan

Daniel M. Sullivan Examiner AU 1636 Room: 12D12 Mail Box: 11E12 Tel: 703-305-4448

Searcher:	
Phone:	
Location:	
Date Picked Up:	
Searcher Prep/Review:	
Clerical:	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

/ENDOR/COST (wi	here applic.)
STN:	
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U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's	· same	• • •	Serial
Name:	·	<u>.</u>	Number:
Date:	Phone:		Art Unit:
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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.

Copyright

frame_plus_n2p model

protein search, using

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Run on: Σ

9, 2003, 12:44:53

US-09-914-191-1 1096

Title: Perfect score:

Sequence:

Scoring table:

hits satisfying chosen parameters: 908470 seqs, 133250620 residues

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Total number

Searched:

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Xgapext Ygapext Fgapext Delext

BLOSUM62 Xgapop 10.0 , X Ygapop 10.0 , Y Fgapop 6.0 , F Delop 6.0 , D

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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-MODEL=frame+ ntp, model -DEV=xlp
-MODEL=frame+ ntp, model -DEV=xlp
-MODEL=frame+ ntp, model -DEV=xlp
-DES-A Geneseq 101002 -QFMT=fastan -SUFFTX=rag -MINMATCH=0.1 -LOOPGL=0
-LOOPEXT=0 -UNITS-bite -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS-bite -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -TR MAX=100 -THR MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=ptc -NOFM=ext -HEARSIZE=500 -MINLEN=0 -ALIGN=15
-NOFM=CAL -OUTFMT=ptc -NOFM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRE=USPS914191 @CGN 1 1 114 @runat 09072003 112348 12858 -NCPU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NEG-SCORES=0 -WAIT -DSPELOCK=170 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMEOUT=0 -THREADS=1 -XGARPOF=10 -XGARPEXT=0.5 -FGARPOP=6
-FGAREXT=7 -YGARPOP=10 -YGARPEXT=0.5 -DELOP=6 -DELEEXT=7
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                                                                                                                    AAM38811 standard; Protein; 298
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25-APR-2000, 2000US-0552117.
9-JUL-2000, 2000US-059842.
19-JUL-2000, 2000US-062312.
03-AUG-2000, 2000US-0653450.
14-SEP-2000, 2000US-0662191.
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Wang Z, Wehrman T,
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                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 (111-length cDNAs defined in the specification. Where a primer set compises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the price control and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for AMH13628 and AMH13631 to AMH3631 represent human cDNA sequences; AMB92446 to AMH3632 crepresent human amino acid sequences; AMB92446 to AMH3632 crepresent in the present in the exemplification of the present enead in the exemplification of the present enead in the exemplification
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                                                                                                                     Yamamoto J;
                                                                                                                    Saito K, Ya
, Otsuki T;
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                     Claim 8; SEQ ID 15324; 2537pp + CD ROM; English.
                                                                                                                                  Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                     Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
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                                                                                                                    Isogai T, Nishikawa T,
            29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-RAX-2000; 2000JP-02418999.
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49.23%
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                                                                                           (HELI-) HELIX RES INST
                                                                                                                                                           WPI; 2001-318749/34.
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Best Local Similarity:
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                                                                                                                                  Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598
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DB:
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ઠે 유 8 셤 ઠ 셤 ò В ð

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The invention relates to human nucleic acids (AAIS7798-AAI61169) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypucleotide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disgnosis and therapy, drug screening, as assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assays for receptor activity, arthritis and initalmination, revocation C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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Zhang J;
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Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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Claim 8; SEQ ID 13475; 2537pp + CD ROM; English.

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                                                                                                                                                                                                                                                       ValProLeuHisCysAspileIleGlyAspAlaPheTrpLysGluHisProGluIleLeu 294
                                                                                          CAACAATCTGGACTAACACCCAGGTACAAGCCCCAAGGGAGATTACAGGGAACTCTTNCAGCA
                                                                                                     GACAAGAATGAGATTTTGTTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATG
                                                                                                                                          AsplysasnGlulleLeuPheSerGluPheAsnIleAsnTyrAsnAsnGluLeuProMet
                                                                                                                                                                               AAGCTGCCAACAGAAATGGAAGGAAAAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCA
                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                    detection; diagnosis; antisense therapy; gene therapy
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, Otsuki 1
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103
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      Length:
Matches:
Conservative:
Mismatches:
Indels:
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Wakamatsu A, Nagai K,
                                                      Gaps:
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                                                                         (1-298)
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                                                                          x AAM38811
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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       5.7e-52
544.00
99.04%
99.04%
49.23%
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                                                                        US-09-914-191-1 (1-598)
                       Percent Similarity:
Best Local Similarity:
Query Match:
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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Alignment Scores:
Pred. No.:
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Ishii S,
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The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligounclectide complementary
to the complementary strand of a polynuclectide which comprises one of
the 5602 nuclectide sequences defined in the specification, where the
oligonuclectide comprises at least 15 nuclectides; or (b) a combination
of an oligonuclectide comprising a sequence complementary to the
complementary strand of a polynuclectide which comprises a 5'-end
sequence and an oligonuclectide comprises a 3'-end sequence complementary to the
complementary strand of a polynuclectide which comprises a 1'-end sequence to sequence complementary to a
polynuclectide which comprises a 3'-end sequence to sequence therefore
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
in gene therapy. The primers are useful for synthesising polynuclectides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH0316 to AAH13628 and
AAH13633 to AAH18742 represent human cDNA sequences;

AAH13633 to AAH18742 represent human cDNA sequences;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479
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                                                                                                                                                                                                                                                                                                                                                                                                            AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 CAACAATCTGGACTAACACCAGTACAAGGCCAAGGGAAGTTACAGGGAACTCTTNCAGGA
195 GlnGlnSerGlyLeuThrProValGlnAlaGlnGlyArgLeuGlnGlyThrLeuAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AspLysAsnGluIleLeuPheSerGluPheAsnIleAsnTyrAsnAsnGluProProMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 TyrArgLysGlyThrValLeulleTrpGlnLysValAspGluValMetThrLysGlulle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysLeuProThrGluMetGluGlyLysLysMetAlaValThrArgThrArgThrLysPro
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Matches:
Conservative:
Mismatches:
Indels:
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537.00
98.08%
98.08%
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Best Local Similarity:
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AAM40597 standard; Protein; 297 AA
WPI; 2001-442253/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAIS9753
                                                                                                                                                                                                                                                                                                                       WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification
                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                 22-OCT-2001
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Pred. No.:
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                                                                                                                                                                                                                                                                 leukaemia.
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Wang J, V
Zhao QA,
                                                                                                      AAM40597;
                                                                                                                                                              Нишап
                                                            AAM40597
                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                    AAH32943 to AAH31195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient of genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated PB, by inserting the nucleic acids into a host cell and culturing the cell cancer and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGACAAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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Mismatches:
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Matches:
                                                                                                                                                                                                        Rosen CA;
                                                                                                                                                                                                                                                                                                                       Claim 11; Page 6911-6912; 9803pp; English
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                                                                                                                                                                                                        Birse CE,
                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                 99US-0157137.
                                                                                                    28-SEP-2000; 2000WO-US26524
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100.00%
100.00%
41.18%
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N-PSDB; AAH33902.
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                                             WO200122920-A2.
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                                                                                                                                 29-SEP-1999;
                Homo sapiens
                                                                                                                                               03-NOV-1999;
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Auntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed
                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-CTT-2000; 2000US-0633036.
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427.00
                                                                        polypeptide SEQ ID NO
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(first entry)
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capable of detecting 1000 or more genes from Drosophila. The invention i useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL20511), expressed DNA sequences (ABL50175) and the encoded proteins (ABB57777-ABP27072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATCTGGACTAACACCCAGGTACAAGGCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC
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| LysAsnGluLeuLeuPheGlnGluPheGlyIleAsnTyrAsnAsnLeuProAlaMetTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAAAGGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAG
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-------1leLeuGlyGluLys------SerArgGlnAlaValVal
                                                                                                                                                                                                                                                                                                                                                                                        AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT
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47
13
21
18
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Matches:
Conservative:
Mismatches:
Indels:
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219.00
60.61%
47.47%
19.82%
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99US-0123180.
99US-0123548.
99US-0126264.
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99US-0126264.
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                                                                                                                                                          286 AA;
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Best Local Similarity:
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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05-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                    ---- 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                 GACAAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATG
                                                                                                                                                                       283 CysLysProSerHisLeu-------
                                                                                                                                                                                                                                                                                                                                                                                      CTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTGGTGTGTTAACCATGCAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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    Conservative:
Mismatches:
Indels:
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                                          Gaps:
                                                                        (1-297)
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                                                                      US-09-914-191-1 (1-598) x AAM40597
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11-JUL-2000; 2000US-0614150.
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genes from Drosophila and
  67.42%
67.42%
38.64%
22
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Percent Similarity:
Best Local Similarity:
Query Match:
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990S - 01513758

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990S - 01517773

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99US-0144333.
99US-0144334.
99US-0144335.
                    20-JUL-1999;
20-JUL-1999;
20-JUL-1999;
21-JUL-1999;
21-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
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31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
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22-JUL-1999;
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13-AUG-1999;
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17-AUG-1999;
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      termination sequence.
                                            Arabidopsis thaliana
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                                                                                                                         06-SEP-2000
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143 LysSerGlyLysSerValSerGluThrGlnGluIleLeuLysAspThrGlnLysGlnGln 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               475 AGGAAAGGGACTGTTGATATGGCAGAAGGTGGATGAAGTGATGATGACAAAGAAATTAAG 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595 CAATCTGGACTAACACCCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 CTGCCAACAGAAATGGAAAGAAGAAGATGGCAGTGACCCGGACCAAGGCCAGTG 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 48412.
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32
21
40
9
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Conservative:
Mismatches:
Indels:
Gaps:
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99US-0159295.
99US-0159329.
99US-0159330.
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99US-0160814.
99US-0160815.
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129.50
51.96%
31.37%
11.72%
                                                                              99US-0159637
                                                                                                 99US-0159638
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99US-0160741
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Best Local Similarity:
                                                        14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
21-OCT-1999;
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203 ------LysHisAspGluAsnGlyAsnProValLysArgLeuArgArgLysAlaVal 219
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990S-0146388
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990S-0151086
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31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
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	Length: 502 Matches: 32 Conservative: 21 Mismatches: 40 Indels: 9 Gaps: 2	1 (1-598) x AAG39160 (1-502) CAATCTGGACTAACACCAAGGCAGAGGAGATTACAGGGAACTCTINCAGCAGAC 536 :::
99US-0153070 99US-0154018 99US-0154018 99US-0154779 99US-0155139 99US-0155139 99US-015555 99US-015555 99US-015675 99US-015675 99US-015923 99US-015923 99US-015923 99US-015923 99US-015924 99US-015928 99US-015981 99US-015981 99US-015981 99US-015981	1.52e-05 129.50 : 51.96% :ity: 31.37% 11.72%	-598) x AAG39160 CTGGACTAACACCAGT ::: erGlyLysSerValSe ATGAGATTTGTTTTC snGl :: snGluLeuLeuPheGl AAGGGACTGTGTTGTT :: :: 1nGlySerCysLeuPh
113-SEP-1999 113-SEP-1999 120-SEP-1999 220-SEP-1999 220-SEP-1999 220-SEP-1999 230-SEP-1999 240-SEP-1999 250-SEP-1999 260-S	ment Scores: No.: nt Similarity Gocal Similar Match:	-914-191- 595 148 . 535 . 168
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99US-0139454.
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99US-0139461.
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99US-0140854.
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99US-0148341.
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99US-0147260
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99US-0144884
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                18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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                                                                                          -JUN-1999
   220 PheValHisSerGluAsnIleAlaGlyArgSerPheTrpAsnGluGlnProSerLeuTyr 239
                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 48411.
                                                       AAG39159 standard; Protein; 520 AA
                                                                                                                                                                                            99US-0121825.
99US-0123180.
99US-0125788.
99US-0125788.
99US-0126785.
99US-0126785.
99US-012834.
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99US-0132484.
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99US-0134256.
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990S - 0.134219
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990S - 0.134768
990S - 0.134941
990S - 0.135124
990S - 0.135529
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99US-0139119.
99US-0139452.
99US-0139453.
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                                                                                18-OCT-2000 (first entry)
                                                                                                                                       Arabidopsis thaliana.
              298 GATGAA 293
                       240 AsnAsp 241
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28-APR-1999;
30-APR-1999;
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19-APR-1999;
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23-APR-1999;
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01-APR-1999
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                                                                    AAG39159;
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356

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595 CAATCTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC 536
                             355 CCCTTGCACTGCGAT---ATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTA 299
                                                                                                                                              475 AGGAAAGGGACTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAG 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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221 ------LysHisAspGluAsnGlyAsnProValLysArgLeuArgArgLysAlaVal
                                                                        535 AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT
                                                                                                                                                                 415 CTGCCAACAGAAATGGAAGGAAAAAAAGATGGCAGTGACCCGGACCAAGGCCAGTG
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99US-0123180.
99US-012348.
99US-0126264.
99US-0126285.
99US-0128234.
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99US-0134218.
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99US-0134221.
99US-0134370.
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99US-0129845.
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99US-0132407
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99US-0132863
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29-MAR-1999;
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990S - 0148684 - 990S - 0149684 - 990S - 0149175 - 990S - 0149175 - 990S - 014972 - 990S - 014972 - 990S - 014992 - 990S - 014992 - 990S - 014992 - 990S - 014993 - 990S - 015993 - 990S - 015193 - 990S - 015
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51.96%
31.37%
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Best Local Similarity:
                                                  18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
24-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
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Pred. No.:
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Query Match: DB:

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18-MAY-1999; 19-MAY-1999; 20-MAY-1999; 21-MAY-1999; 24-MAY-1999;						18-JUN-1999; 18-JUN-1999;					18-JUN-1999;		22-JUN-1999; 23-JUN-1999;					02-JUL-1999; 06-JUL-1999;				16-JUL-1999;							JUL-1999;			22-JUL-1999;		25-JUL-1999; 26-JUL-1999;	1 444 T-700-17
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                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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399 LysAsnGluLeuLeuSerGlnGlnPheGlyIleGluTyrAsnSerLeuProValllePhe
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 61881.
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                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
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99US-0161993.
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99US-0123180.
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                                                                    2.2e-05
128.00
56.57%
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Best Local Similarity:
26-OCT-1999;
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28-OCT-1999;
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05-MAR-1999;
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21-APR-1999;
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535 AAGAATGAGATTTTGTTTTCTGAATTCCAACATCAACTATAATAATGAGCTGCCGATGTAT 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Mismatches:
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12 - 70L - 1999; 13 - 70L - 1999; 14 - 70L - 1999; 16 - 70L - 1999; 16 - 70L - 1999; 19 - 70L - 1999; 20 - 70L - 1999; 20 - 70L - 1999; 21 - 70L - 1999; 99US-0154039. 99US-0154779. 99US-0155139. 99US-0155486. 99US-0155659.

> 23-SEP-1999; 24-SEP-1999; 28-SEP-1999;

27-AUG-1999 27-AUG-1999 30-AUG-1999 01-SEP-1999 01-SEP-1999 11-SEP-1999 11-SEP-1999 15-SEP-1999 16-SEP-1999 20-SEP-1999 22-SEP-1999

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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value sequences are actor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCACCCCGTTCCATC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTCTCATTCGCACCAGTGTCCTGGGTG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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-----LysGlyAlaMetValGlyIleAlaIleGlyGlyGlyPheValLeuLe
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                    Herbicidally active polypeptide SEQ ID NO 1632.
                                                                     Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                                                                  28-AUG-2001; 2001WO-EP09892
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38.89%
30.56%
8.26%
                                                                                                                                                                                                                                                                                                                                                                                                                 Tietjen K, Weidler M;
                                                                                                                   Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            694 AA;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG.
                                                                                                                                                                    WO200210210-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gnment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 AGGAAAGGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCCAACAGAAATGGAAGGAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AsnGlyGluValSerGlyLysGlnVal--------GluAlaGluValGly 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .:: :::|||||| |||||| ValAspTyrSerAsnileIleAspGlnCysPheTrpGlnGlnHisProHisIleLeu 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||||||::|||
LysAsnGluLeuLeuSerGlnGlnPheGlyIleGluTyrAsnSerLeuProValIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT
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Matches:
Conservative:
Mismatches:
Indels:
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                                                             990S - 015786S - 990S - 015786S - 990S - 0158329 - 990S - 0158389 - 990S - 0159294 - 990S - 0159339 - 990S - 0159331 - 990S - 0159531 - 990S - 
                                                                                                                                                                                                                                                                                                             990S-0159637
990S-0159638
990S-015984
990S-0160741
99US-0160767
99US-0160768
99US-0160814
99US-0160815
99US-0160815
99US-0160815
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99US-0161405.
99US-0161406.
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128.00
56.57%
32.32%
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Best Local Similarity:
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21-0CT-1999
22-0CT-1999
22-0CT-1999
25-0CT-1999
25-0CT-1999
25-0CT-1999
25-0CT-1999
25-0CT-1999
25-0CT-1999
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99US-0139459.
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99US-0139460.
99US-0139462.
99US-0139463.
99US-0139463.
99US-0139750.
99US-0139750.
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990S-0146389.
990S-0147038.
990S-0147204.
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99US-0140353.
99US-0140354.
99US-0140695.
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99US-0142154.
99US-0142055.
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99US-0142803.
99US-0142920.
99US-0142977.
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99US-0140991.
99US-0141287.
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99US-0145913.
99US-0145918.
99US-0145919.
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99US-0147260.
99US-0147303.
99US-0147416.
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99US-0147935.
99US-0148171.
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18-AUG-1999;
20-AUG-1999;
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                                                                                                                                                                                                                                6-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                           3-JUL-1999
                                                                                          Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 75712.
                         AAG58628 standard; Protein; 128 AA
                                                                                                                                                                                            99US-0121825.
99US-0123180.
99US-0123180.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0126785.
99US-0126786.
99US-0126786.
99US-0130871.
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990S-0137528
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990S-0138094
990S-0138847
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990S-0139119
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990S-0139454.
990S-0139455.
990S-0139456.
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                                                         18-OCT-2000 (first entry)
                                                                                                                           Arabidopsis thaliana
                                                                                                                                          EP1033405-A2
                                                                                                                                                             06-SEP-2000
                                         AAG58628;
       RESULT 14
AAG58628
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us-09-914-191-1.rag

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The differentiation enhancing factors (DEF), comprise at least one each of SH3 consensus binding sequence, ankyrin repeat, pleckstrin homology domain and C2 domain. The DEF induce adipogenesis or neurogenesis; they are mediators of SH3-domain dependent signalling and may be involved in cellular gene expression, cytoskeletal architecture, protein trafficking, endocytosis or adheshon, migration, proliferation and differentiation of cells. Typical applications of DEF and agents that modulate cells or expressing them, are treatment of hyperplastic and neoplastic disease (a wide range of solid tumours and leukaemias), including metastases; for in vitro induction of differentiation of neural crest cells to neurons, of plaid cells etc.; for increasing neuron survival, and inducing cell repair, in the nervous system (e.g. treatment of traummatic injury, stroke, Alzheimer's, Parkinson's or Huntington's diseases, amylotrophic lateral sclerosis, multiple sclerosis etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zebrafish, differentiation enhancing factor, ankyrin repeat, C2 domain, SH3 consensus binding sequence; pleckstrin homology domain; adipogenesis; neurogenesis; hyperplastic disease; neoplastic disease; nervous system.
                                                193 GGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGCTTGCATGG 252
                                                                                                           253 TTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGAT 312
                                                                                                                                                                          313 GTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGGCAAAGGGCA---CTGGCTTTGTCC 369
49
                                                                                                                            69 ArgProGluLysLysGlnSerAspLysSerAsnTyrAlaArgAlaGluLeuPheArgGly 88
                                                                             ----LeuLeuTrp
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for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding differentiation enhancing factor - particularly to regulate adipogenesis and neurogenesis, e.g. treating tumours and neurological disease
                                                                                                                                                                                                                                                                                                                                                                                                                          Zebrafish differentiation enhancing factor 2 protein.
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                                                                                                                                                                                                                                                                                                                               AAW77288 standard; Protein; 982 AA.
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                                                                                                                                                                                                                                      370 TGGTCCGGGTCACTG 384
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                                                                             SerArgGlnThr----
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SH3 consensu
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Mismatches:
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                                                                         99US-0150884.
99US-0151065.
99US-0151066.
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99US-0156458.
99US-0156596.
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99US-0159637.
99US-0159638.
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99US-0160814.
99US-0160815.
99US-0160980.
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99US-0160989.
99US-0161404.
99US-0161406.
99US-0161369.
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99US-0161992.
99US-0161993.
99US-0162142.
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99US-0157753.
99US-0157865.
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99US-0151438
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99US-0154018
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99US-0154779
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99US-0159293
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99US-0160767
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31.43%
8.07%
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Best Local Similarity:
                                                                          26-AUG-1999
                                                                                            27-AUG-1999
                                                                                                         27-AUG-1999
27-AUG-1999
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                                                            25-AUG-1999
                                                                                                                                                                                       07-SEP-1999
                                                                                                                                                                                                       10-SEP-1999
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85 AACAAGGTGTTCTGCTTAAAC-----AGAGTAAGATACACCACCCCCATCCAT 132

US-09-914-191-1 (1-598) x AAG58628 (1-128)

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133 CCCTTCCTTCCCTGTTCCCCTCCCACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGT 192 :::|||
3 SerlysalalleCysLeuGlyPheLeuProProArgLeuArgPheSerSerProArgLeu

Sequence 982 AA;

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389 GATGGCAGTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGG--- 333
                                                                                                                                                                              ----TCCAGA 306
                                                                                                                                                                                                     719 IleSerCysTyrThrProGlySerAsnSerLeuGlnLeuSerProAlaSerLeuSerArg 738
                                                                                                                                                                                                                            305 GATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTGGT------ 261
                                                                                                                                                                                                                                                    739 AspGlyArgAspLeuValLysAspLysGlnArgPheValProAsnLeuValAsnAsnGlu 758
                                                                                                                                                                                                                                                                                                                                              778 ------ProLeuProProArgAsnLeuValGlnProSerAlaLeu---AlaGly 792
          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                             332 ---GGATGCTTTCTGGAAGGAACA----
                                                                                               US-09-914-191-1 (1-598) x AAW77288 (1-982)
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           4.33
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Scoring table:

Minimum DB seq Maximum DB seq Total number

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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart.D.
APPLICANT: Puranam, Kasturi
APPLICANT: Stuart
APPLICANT: APPLICANTION COMPOSITIONS ON DISCASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: 1999-12-14
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Mismatches:
Indels:
           US-09-108-020-43
US-08-952-9813-2
US-08-913-9813-2
US-08-914-917-32
US-08-915-856-32
US-08-314-977-36
US-08-314-977-36
US-08-314-977-14
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US-08-315-850-3
US-08-914-6865-14
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US-08-914-6865-14
US-09-915-850-14
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 389, Application US/09461697; Patent No. 6277974; GENERAL INFORMATION:
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76.00
33.70%
26.09%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
RESULT 1
US-09-461-697-389
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TYPE: PRT
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10, Appl
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Sequence 375, App
                                                                                                  9, 2003, 12:46:48; Search time 13.5 Seconds (without alignments) 2606.653 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                     protein search, using frame_plus_n2p model
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US-09-461-697-375
US-09-66-697-373
US-09-006-285A-10
US-08-097-6
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
STRESP FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
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Conservative:
Mismatches:
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APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NOWER: US/09/461,697
CURRENT APPLICATION NOWER: US/09/461,697
SOFTWARE: FASTESE for Windows Version 4.0
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Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Mallace L.M.
                                                                                                                                                    Sequence 373, Application US/09461697; Patent No. 6277974; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-914-191-1 (1-598)
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Query Match:
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US-09-056-285A-10
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Pred. No.:
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Barney. Shawn
APPLICANT: Barney. Stawn
APPLICANT: Partey. Stawt D.
APPLICANT: Puranam, Kasturi
APPLICANT: Nan TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                            -----TGTTGGCAG 415
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|GluAlaAspArgAspIleMetThrLeuAlaAsnHisTrpAsnCysProValLeuSerSer
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                         CTTAATTTCTTTTGTCATCACTTCATCCAC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 375
LENGTH: 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
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Patent No. 6277974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTC----
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33.70%
26.09%
6.93%
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Best Local Similarity:
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231 sGlyAlaLeuValrrp 236
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                  CGGTGTTGGAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.54%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304-1018
                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hammon
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
MOLECULE TYPE: |
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 GluhlaGluGluGlyLeuGlnGlyGlnLeuGlyAlaLeuArgArgGluArgAspGlnLeu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 GAGATITIGITITICIGAATICAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 GluThrGlnThrArgAspLeuGluAlaAlaTyrAsnAsnLeuLeuArg----- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 GGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAGCTGCCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:::
-----AspLysSerAlaLeuGluGluGluLysArgGln 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GTGACC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 LeuGluGlnGluAsnGluAspLeuAlaArgArgLeuGluSerSerSerGluGluValThr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 CGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATA---TCATCGGGGATGCTTTCTGG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 A---AGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 ySerArgGluValSerGlnTrp-----AsnLeuAspThrLeuAlaPheGln---- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTGCTTAACCATGCAAGCCCTCCCACCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCCCTACCACCCAGGACACTGGTGCGAATGACACAACTCAAGTTGGGAGGGGAACAGG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 uValProAlaSerGlnIleLeuLysGluAsnProSer-----GlyArgProArgSe 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --Cy 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GluLeuLysSerGluLeuThr-----
                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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4490
640
630
100
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                     NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-056-285A-10
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                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                         TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                               ZIP: 02109-2170
COMPUTER READABLE FORM:
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CITY: Boston
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Best Local Similarity:
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93 Glu--------GlyvalTyrLysCysLeuHisTyrSerAspSerValSer 106
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                                                           550 ACTCTINCAGCAGACAAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAAT 491
                                                                                                                                       490 GAGCTGCCGATGTATAGGAAAGGGACTGTTGATATGCCAGAAGGTGGATGAAGTGATG 431
                                                                                                                                                                                                                                                                                                                                                                              310 CCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTGGTGTTTAACC 251
                                                                                     250 ATGCAAGCCCTCCCACCTCCCAGGGCTCCTTGCCTTAGGTGGCTG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --IleThrTrpLeu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Targetable Vector Particles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,126
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 MetArgSerLysProProFroGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRILING DATE: 08/326,347
FILING DATE: 20-0CT-1994
APPLICATION NUMBER: 08/973,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARFILING DATE: 09-NOV-1992
FILING DATE: 09-NOV-1992
NAME OF THE OFFICE OF THE OFFICE OFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inch diskette
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Patent No. 5985655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Anderson, W. French
APPLICANT: Baltrucki, Leon F.
APPLICANT: Mason, James W.
TITLE OF INVENTION: Targetable
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carella, Byrne,
Cecchi, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 Becker Farm Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lillie, Raymond J
REGISTRATION NUMBER: 31,
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ADDRESSEE: Carella, F
ADDRESSEE: Cecchi, St
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
COMPUTER: IBM PS/2
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: New Jersey
RY: USA
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     137 -----
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772 AlaAlaArgMetLeuAsnLeuThrProAlaAspIleThrAlaCysHisLeuGlnGlnLeu 791
                                                                                                                                                                                                                                                               330 TCCCCGATGATATCG------CAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGG 377
                                      754 ThrSerAlaileAlaAsnMetPheThrCys-----AsnHisThrProlleArgSerCys 771
                                                                               378 GTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bazan, J. Fernando
PEPLICANT: Zlotnik, Albert
TITLE OF INVENTION: PURIFIED MAMMALIAN T CELL ANTIGENS AND
TITLE OF INVENTION: RELATED REAGENTS
TOWBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
219 CAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACC
                                                                                                                                                                               393
34
116
46
39
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Mismatches:
                                                                                                                                                                                                                                                                                                                                               US-09-914-191-1 (1-598) x US-08-429-742-2 (1-393)
                                                                                                                                                                                                                                                                                                                    438 TCATCCACCTTCTGCCATATCAACACAGTC 467
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901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/429,742
FILING DATE: 26-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ching, Edwin P. REGISTRATION UNMERR: 34,090
REFERENCE/DOCKET NUMBER: DX0505
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08429742
Patent No. 5686257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kennedy, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
LENGTH: 393 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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US-08-429-742-2
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Query Match:
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---CCAGTACAAGCCCAAGGGAGATTACAGGGA 551

592 TCTGGACTAACA----

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; Sequence 395, Application US/09461697; Patent No. 6277974; GENERAL INFORMATION:
                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lingenfelter, Susan
REGISTRATION NUMBER: P-41,156
REFERENCE/DOCKET NUMBER: 95-31
TELEPHONE: 206-442-6675
                                                                                                                                                                                                                                                                                                                           : 1012 amino acids
amino acid
                                                                                                                                                                                                                                                                                  TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                          single
   COMPUTER READABLE FORM:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                       113 GATACACCCCCCATCC------ATCCCTTCCTTCCTGTTCCCTC 154
                                                                                                                                                                                                                                                                 155 CCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGTGGTAGGATGCTACAGCCACCT 214
                                                                                                                                                                                                                                                                                                                          215 AAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAACTGAAGC 274
                                                                                                                                                                                                                                                                                                                                                                                    367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 Asp-----LysThrGlnGluCysTrpLeuCysLeuValSerGlyProProTyrTyrGlu 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 TITICCTICCATITCTGTIGGCAGCTIAATTICTITIGICATCACCITCACCACCTICIG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 AlaserGlnHis-----LysLeuThrLeu-SerGluValThrGlyGlnGlyLeuCy 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 CCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGAA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LeuCysAs 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 ITCAGAAAACAAAATCTCA------TTCTTGTCTGCTGNAAGAGTTCCCTGTAA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CCTGGTCCGGGTCACTGCCATCTT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                            335 GATGATATCGCAGTGCAAGGGCACTGGCTTTGT-------
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s---ValGlyAlaValProLysThrHisGlnAla------
                                                                                                   Conservative:
Mismatches:
Indels:
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| ProSerGlyThrValSerMetValProGlyAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           560 TCTCCCTTGGGCTTGT---ACTGGTGTTAGTCCA 590
                                                                                                                                                                          US-09-914-191-1 (1-598) x US-08-484-126-3 (1-453)
                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                xenotropic gp70 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------
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Patent No. 6300093
                                                                                   72.50
33.85%
22.92%
6.61%
                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98102
               NAME/KEY:
                                                        Alignment Scores:
                           US-08-484-126-3
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FEATURE:
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129 CCATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCT 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 ATGGTTAAGCACCACAGAACTGAAGCGCAAAAG------GGTCAGCTGTCTTCATCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 ProAlaAlaProSerSerValPro-------HisGlyArgGlnLeuPro 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 GlyArgLeuGlyCysLeu----LeuGluGluGlyLeuCysGlyAlaSerGluAlaCys 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 ValAsnAspGlyValPheGlyArgCysGlnLysValProAlaMetAspPheTyrArgTyr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Actual, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette
CONFUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/811,481
FILING DATE:
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LENGTH: 247
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TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-99
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: PSAESEQ for Windows Version 4.0
SEQ ID NO 395
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TGTTGGCAGCTTAATTTCTTTTGTCAT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 CACTTCATCCAC------CTTCTGCCATAT------CAA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 IleLysGlyThrGlnAsnTyrIleProAlaLysCysPheSerLeuAspAlaPheCysHis 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetThrLeuAlaAsnHisTrpAsnCysProValLeuSerSerAspSerAspPheCysIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 PheAspLeuLysThrGlyPheCysProLeuAsnSerPheGlnTrpArgAsnMetAsnThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 ------GGTCCGGGTCACTGCCATCTTTTTTCCTTCCATTTC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08463911

Patent No. 5869330

GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCE: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                         375
22
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6
18
40
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APPLICATION NUMBER: US/08/463,911
                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                   US-09-914-191-1 (1-598) x US-09-461-697-395 (1-375)
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                                                                                                                                                                                                                                                                                                                                                                                                                     341 ATCGCAGTGCAAGGGCACTGGCTTTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-norman SOFTWARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 HisValAsnLeuProlle 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
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                                                                                                                                                                                                                                                         4.89
72.00
32.56%
25.58%
6.57%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-461-697-395
                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
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241 CTCCCACCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAGCAT---CCCTACCACCAGGA 185
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                                                                                                                                                                                                                                                                                                                                                                                                          32 ValbroProProLysGlyThrCysAlaGlyTrpWetAlaGlyIleProGlyHisProGly 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::||||||||:::
32 ValProProProLysGlyThrCysAlaGlyTrpMetAlaGlyIleProGlyHisProGly 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 His--------AsnGlyThrProGlyArgAspGlyArgAspGly 63
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Patent No. 6197930

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOWOLOGS
FILE REFERENCE: 97-49

CURRENT APPLICANTON WIMBER: US/09/140,804

CURRENT FILING DATE: 1998-08-26

EARLIER APPLICATION NUMBER: 60/056,983

EARLIER FILING DATE: 1997-08-26

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                     Length:
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US-09-118-408-3
Sequence 3, Application US/09118408A
; Patent No. 6265544
; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
                                                                                           : 247 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.42
71.00
51.28%
38.46%
6.43%
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71.00
51.28%
38.46%
6.43%
                                                                                                                                            ; MOLECULE TYPE: protein US-08-463-911-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                 linear
                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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                                                                                                                               TOPOLOGY:
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Sequence 43, Application US/09108020A

Patent No. 6143561

GENERAL INFORMATION:

APPLICANT: Randall, Douglas D.

APPLICANT: Monston, Mark L.

APPLICANT: Money, Brian A.

APPLICANT: Meerly, Jan A.

APPLICANT: Money, Brian P.

TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE AND

TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE AND

TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE TOO

TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE OF THE REFERENCE: US/09/108,020A

TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE OURRENT APPLICATION NUMBER: 60/051,291

EARLIER PILING DATE: 1999-06-30

EARLIER PILING DATE: 1997-06-01

EARLIER PILING DATE: 1997-06-01

EARLIER PILING DATE: 1999-08-01

EARLIER PILING DATE: 1999-03-02

NUMBER OF SEQ ID NOS: 54

SOUTWARE PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||||
150 ThrProTyrAsnAlaLysGlyLeuLeuLysSerAlaIle---ArgAspAsnAsnProVal 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ATGTATAGGAAAGGG-----ACTGTGATA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 TyrSerArgMetArgHisHisValThrGluAlaLeuProLeuLeuLeuAsnAspGlyTyr 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 ServalLysLysThrHisArgValLeuIleValGluGluCysMetLysThrAlaGlyIle 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 ACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAATGAGATT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 CACTGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 AGCTGACCCTTTTGCGCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCCACCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 TIGITITICIGAATICAACAICAACIATAAT----AAIGAGCIGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 TGGCAGAAGGTGGATGAAGTGACAAAAGAAATTAAGCTG----
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652
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Mismatches:
Indels:
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71.00
39.38%
21.88%
6.43%
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: P. purpurea
US-09-108-020-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
US-09-108-020-43
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US-08-952-981A-2
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DB:
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32 ValProProDysGlyThrCysAlaGlyTrpMetAlaGlyIleProGlyHisProGly
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-----AsnGlyThrProGlyArgAspGlyArgAspGly 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 13
S-09-506-855-3
S-09-506-855-3
S-09-606-855-3
Patent No. 644821
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sheppard, Faul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
              TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS FILE REFERENCE: 97-30
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Matches:
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Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
                                              CURRENT APPLICATION NUMBER: US/09/118,408A CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                          Gaps:
APPLICANT: Sheppard, Paul O.
                                                                                                                                                                                                                                                                               5.42
71.00
51.28%
38.46%
6.43%
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51.28%
38.46%
6.43%
                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-118-408-3
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ORGANISM: Homo sapien
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Best Local Similarity:
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Best Local Similarity:
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RESULT 14

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| 1239 GlyProLysThrCysSerAsnThrTrpHisGlyThrPheProlleAsnAlaTyrThrThr 1258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 ---AGCTGCCAACAGAAATGGAAGGAAAAAAAGATGGCAGTGACCGGACCAGGACAAAGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 TAGATGAAGACAGCTGAC------CCTTTTGCGCTTCAGTTCTGGTGTGCT 256
                                                   APPLICANT: DE FRANCESCO, Raffaele
APPLICANT: TOWEL, Licia
APPLICANT: TOWEL, Licia
APPLICANT: BERRENS, Sven-Erik
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE RNA-DEPENDENT RNA
TITLE OF INVENTION: POLYMERASE AND TERMINAL NUCLECTIDYL TRANSFERASE
TITLE OF INVENTION: ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
FILE REFERENCE: ITOOORD
                                                                                                                                                                                                                                                                                                                                                                                                    2201
24
13
33
19
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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|1259 GlyProCysThrProSerProAlaPro 1267
                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/952,981A
CURRENT FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 TAACCATGCAAGCCCTCCCACCTCCCA 229
Sequence 2, Application US/08952981A Patent No. 6383768 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: CDNA clone pCD (38-9.4)
US-08-952-981A-2
                                                                                                                                                                                                                                                                                                                                                                                                    15.2
70.50
41.57%
26.97%
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Best Local Similarity: 2
Query Match:
DB:
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LENGTH: 2201
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Search completed: July 9, 2003, 12:51:58 Job time : 19.5 secs

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Sequence: Title: Perfect s

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Run on:

Scoring table:

Total number

Searched:

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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid
FILE REFERENCE: PAOGSP1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR FPLICATION NUMBER: US/US00/26524
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-38
NUMBER OF SEQ ID NOS: 8564
                                    Sequence 373, App
Sequence 174, App
Sequence 117, App
Sequence 107, App
Sequence 107, App
Sequence 11, App
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 1311, Appl
                                                                                                                                                                                                                                                              Sequence 383, Appl
Sequence 3, Appl
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 6, Appli
 Sequence 389, Apr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4,
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Sequence 2,
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0 US-09-910-1744-16

0 US-09-955-866-12

0 US-09-815-227-16

0 US-09-815-224-14005

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0 US-09-916-8428-5

0 US-09-916-8428-5

0 US-09-916-8428-7

0 US-09-916-8428-7

0 US-09-788-711A-2

0 US-10-189-971-14

US-10-189-971-14
                                        US-09-922-261-373

US-09-78-240-6

US-09-984-130-144

US-09-925-300-1578

US-10-184-644-107

US-10-184-644-107

US-10-184-641-107
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Matches:
Conservative:
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sapiens
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Percent Similarity:
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US-10-106-698-5245
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TYPE: PRT
ORGANISM: 1
 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
-MODEL=frame+ n2p, model - DEV=x1p
-QODEL=frame+ n2p, model - DEV=x1p
-Q=/Cgn2 1/USFTO_spool/US09914191/runat_09072003_112351_12946/app_query.fasta_1.775
-Q=/Cgn2 1/USFTO_spool/US09914191/runat_09072003_112351_12946/app_query.fasta_1.775
-DB=Published_Applications_AA - QFMT=fastan - SUFFIX=rapb - MINMATCH=0.1
-LOOPCL=0 - LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62
-TTRANS=human40.cdi - LIST=45 - DOCALLGN=200 - THR SCORE=pct - THR MAXEL=0.0
-THR MIN=0 - ALIGN=15 - MODE=LOCAL - OUTFWT=pct - NORM=ext - HEAPSIZE=500 - MINLEN=0
-MAXLEN=2000000000 - USER=US09914191 @CGN 1 1.7 @runat_09072003_112351_12946
-NOFUS=3 - NO WMAP - LANGEQUERY - NGG SCORES=0 - WAIT - DSPBLOCK=100
-LONGLOG - DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=-10 - XGAPEXT=0.5
-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5245, Ap
Sequence 302, App
Sequence 1529, Ap
                                                                                                 ; Search time 31 Seconds
(without alignments)
4491.550 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                       1 ttggaatagttcttgcttta......ggtgttagtccagattgttg
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/ cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/NEO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                     - protein search, using frame plus n2p model
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US-09-844-281-1
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US-09-934-455-302
                                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                            445758 segs, 116419773 residues
                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Y
Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Match Length
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131 ATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGG 190
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305 ThrlleLeuProPheTyrProProProAlaTyrTrpSerCysProGlyValSerProGly 324
                                                                                                                                                                                                                                                       233 AGGTGGGAGGGCTTGCATGGTTAAGCACACCCAGAACTGAAGCGCAAAAGGGGTCAGCTGTC 292
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                                                                                                   285 ValProCysPheProGlyProProProThrTrpProTyrAlaTrpAsnGlyValSerTrp
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Sequence 10.122.
Sequence 10.122020151681A1
Sequence 10. US20020151681A1
Septent No. US20020151681A1
Septent No. US20020151681A1
Septent No. US20020151681A1
Steve Ruben
TITLE NO INVENTION: Nucleic Acids, Proteins and Antibodies.
FILE REFERENCE: PA101
CURRENT FILING DATE: 2001-08-10
PRIOR PRILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                    191 GTGGTAGGGATGCTACAGCCACCTAAGGCAAGG-----
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Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
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LENGTH: 233
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US-09-844-281-1
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ORGANISM:
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                                                                                                                                                                                                                                                          481 ATGTATAGGAAAGGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAA 422
                                                                                                                                                                                                                                                                                       21 MetTyrArgLysGlyThrValLeuIleTrpGlnLysValAspGluValMetThrLysGlu 40
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APPLICANT: Jiang, Cal-Zhong
APPLICANT: Viang, Cal-Zhong
APPLICANT: Rediefe, James
APPLICANT: Rediefe, Oliver
APPLICANT: Rechmann, Jose Luis
APPLICANT: Rechmann, Jose Luis
APPLICANT: Rechmann, Jose Luis
APPLICANT: Pinced, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR PLLING DATE: 2000-08-22
PRIOR PLLING DATE: 2001-01-16
PRIOR PLLING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PATENTING DATE: 2001-04-17
SEQ ID NO 302
THE CALLING DATE: 2001-04-17
SEQ ID NO 302
THE CALLING DATE: 2001-04-17
THE CALLING DATE: 2001-04
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Matches:
Conservative:
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US-09-934-455-302
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APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
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41.18%
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Best Local Similarity:
Query Match:
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Query Match:
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323 GAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCT
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
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Thomas, Mary Beth
Portbury, Stuart D.
Puranam, Kasturi
                     Thomas, Mary Beth
Portbury, Stuart D.
Puranam, Kasturi
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76.00
33.70%
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                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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548 yThrLysThrIleGlyValThrGlyAsnAspValGlyGluGlyThrValHisPheGlnAs 568
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266
448
848
948
Sequence 1, Application US/09844281
Patent No. US20020082386A1
GENERAL INFORMATION:
APPLICANT: Mangold, Beverly L.
APPLICANT: Aldrich, Jennifer L.
APPLICANT: Aldrich, Jennifer L.
TITLE OF INVENTION: Anthrax Specific Antibodies
FILE REFERENCE: 38602.0003
CURRENT APPLICATION NUMBER: US/09/844,281
CURRENT FILING DATE: 2001-04-30
PRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Mismatches:
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Patent No. US20020111471A1
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bacillus anthracis
US-09-844-281-1
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24.86%
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Katz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922,261
CURRENT PILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/461,697
PRIOR PILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Katz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

TITLE OF INVENTION: CELL DEATH
FILE REPRENCE: 10001-005-999

CURRENT APPLICATION UNBER: US/09/922,261

PRIOR APPLICATION NUMBER: US/09/461,697
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APPLICANT: KAEZ, LAWTENCE C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
                                                                                                                                                                                       98 GlualaGinGluGlyLeuGinGlyGlnLeuGlyAlaLeuArgArgGluArgAspGlnLeu 117
                                                                                                                                                                                                                                  529 GAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAA 470
                                                                                                                                                                                                                                                                                                                       469 GGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAGCTGCCA 410
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  Conservative:
Mismatches:
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207 uValProAlaSerGlnIleLeuLysGluAsnProSer-
                                                                                                         x US-09-952-464A-10 (1-490)
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/922,261
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/461,697
PRIOR FILING DATE: 1999-12-14
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Patent No. US20020111471A1
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Puranam, Kasturi
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Barney, Shawn
Thomas, Mary Beth
33.87%
26.34%
6.88%
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ORGANISM: Homo sapiens
                                                                                                         US-09-914-191-1 (1-598)
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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OTHER INFORMATION: Description of Artificial Sequence; No. US20030077587Ale
OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457
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| GlualaaspargaspIleMetThrLeualaasnHisTrpasnCysProValLeuSerSer 127
                                                                                                                                                                                                                                                                                                                                                                                                                                     403
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GGTCCGGGTCACTGCCATCTTTTTTCCTTCCAT
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148 TrpArgAsnMetAsnThrlleLysGlyThrGlnAsnTyrlleProAlaLysCysPheSer
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APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
FILE REPERENCE: 21087.0017011
FILE REPERENCE: 21087.0017011
CURRENT APPLICATION NUMBER: US/09/952,464A
CURRENT FILING DATE: 2001-09-12
PRIOR PILING DATE: 1999-12-18
PRIOR FILING DATE: 1999-12-15
PRIOR PLILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 09/461,542
PRIOR FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: 09/366,952
PRIOR RILING DATE: 1999-08-04
PRIOR RAPLICATION NUMBER: 09/056,285
                                                                                                                                                                                                                                                                                                                                                GAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCT
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                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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PRIOR APPLICATION NUMBER: 08/822,999
PRIOR FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 490
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26.09%
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76.00
                                                                 ORGANISM: Homo sapiens
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Query Match:
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                                                                                                                                                                                       Percent Similarity:
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Pred. No.:
6core:
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SEQ ID NO 375
LENGTH: 488
TYPE: PRT
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718 SerCysGlySerLeuPheProLysAlaLeuGlnArgLeuSerArgSerIleValArgSer 737
                                                                                                                       738 ArgAlaHisSerThrAlaVal------GlyIlePheSerValLeuLeuValPhe 753
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                                                                                                                                                                                                                                                                                                                                          378 GICACIGCCATCITITITCCTITCCATTICTGTTGGCAGCTIAALTITCTTTTGTCATCACT 437
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                                                                                          165 TTGTGTCATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGG-----
                                                                                                                                                       219 CAAGGAGCCCTGGGAGGTGGGAGGCTTGCATGGTTAAGCACACC
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116
139
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APPLICANT: N. 1 c. a. 1.

TITLE CO INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PP489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 06/243,792
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 66/198,407
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-28
NUMBER OF SED ID NOS: 149
SOFTWARE: PATCHTIN VET: 2.0
SEQ ID NO 144
LENGTH: 393
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Mismatches:
Indels:
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 US-09-914-191-1 (1-598) x US-09-750-240-6 (1-1167)
                                                                                                                                                                                                                                                                                                                                                                                                                           826 SerSerValPheLeuHisIleSerSerIle 835
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                                 TCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAG-
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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| IIO GluAlaAspArgAspIleMetThrLeuAlaAsnHisTrpAsnCysProValLeuSerSer 129
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                                                                                                                                                                                                                                                                                                             -------TGTTGGCAG 415
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                                              458 ------CAACACAGTCCCTTTCCTATA 478
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                                             Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
                                                                                                                                                       US-09-914-191-1 (1-598) x US-09-922-261-373 (1-490)
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Gaps:
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                                             23.5
76.00
33.70%
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US-09-750-240-6
                                                             Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
DB:
US-09-922-261-373
                                Alignment Scores:
Pred. No.:
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1138 ---GlyAlaCysThrAlaCysAlaGlyGlyThrGlyCysAlaThrGlyCysCysAlaCys 1156
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357 IGCCCTIGCACTGCGATAICAICGGGGATGCTTICIGGAAGGAACAICCAGAGATICIAG 298
                                                   286 AGCTGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 CACCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAGCATCCCTACCACCCAGGACACTGGT
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                                                                                      ---ArgArgLysSerPro-
                                                                                                                    346 AGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCA 387
                                                                                                                                                      --SerAlaSerGlyLysGlySerArgPro 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: P343OR1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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                                                                                    366 -----MetLysMetĠluLysMet----
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US-10-184-634-107
; Sequence 107, Application US/10184634
                                                                                                                                                                                                                         ; Sequence 107, Application US/10184644; Publication No. US20030044930A1; GENERAL INFORMATION:
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Watanabe, Colin K.
Wood, William I.
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TITLE OF INVENTION: SECRETED
TITLE OF INVENTION: ACIDS EN
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Best Local Similarity:
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                                                                                    -----GlyValTyrLysCysLeuHisTyrSerAspSerValSer 106
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                                                                                                                                                      -----LysValIleValLeuAlaThr 117
                                                                                                                                                                                         311
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                                                                                                                                                                                                                                                                                            ----ValValLeuMetCysSerThr 143
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292 ProArgArgProCysArgSerIleLysGlyAlaTrpLeuCysCysLeuGInSerArgThr 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 ThrArgLeuThrArgProSerThrThrThrPheLeuSerCysSerProPro----Ala 329
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                                                   GAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATG 431
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 310 CCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTGGTGTGCTTAACC
                                                                                                                      144 MetArgSerLysProProProGln------IleThrTrpLeu 155
                                                                                                                                                                                                                                                                                                                             250 ATGCAAGCCCTCCCACCTCCCAGGCTCCTTGCCTTAGGTGGCTG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Clayer Ruben.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAID
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PALENTIN Ver. 2.0
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Patent No. US20020151681A1
GENERAL INFORMATION:
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Best Local Similarity:
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LENGTH: 393
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              TYPE: PRT
CRGANISM: Homo sapiens
US-09-896-738-18
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ORGANISM:
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                                                                                                                                                                             APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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Patent No. US20020165347A1
GENERAL INFORMATION:
APPLICANT: FORCE, Michael
APPLICANT: Fang, Mei
TITLE OF INVENTION: Barlike Molecules and Uses Thereof
FILE REFERENCE: 00-513-A
CURRENT FILING DATE: 2000-06-29
PRIOR FPLING DATE: 2000-06-29
PRIOR FPLING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VEY: 2.0
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US20030068684A1
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Wood, William I.
                                                                                          Godowski, Paul J. Gurney, Austin L.
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35.05%
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                                                                          Goddard, Audrey
                            APPLICANT: Baker, Kevin P.
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ORGANISM: Homo Sapien
                                                                                                                        Pan, James
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Best Local Similarity:
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199 ValGlyLeu-TyrAlaValAlaAlaSerValIleMetArgGlySerSerGlyGlyGlyVa 218
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236 rileAlaAspProPhePheArgSerAlaGlnProTrpIleAlaAlaLeuAlaGlyThr 255
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173 ProGlnProGlnIleLysTrpSer------AspThrLysGlyGluAsnIle
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                                                                                                                                                  US-09-914-191-1 (1-598) x US-09-896-738-18 (1-584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Franch, Stephen T.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. US20
TITLE OF INVENTION: Fanily and Uses Thereof
FILE REFERENCE: 35800/236924
CURRENT APPLICATION WUMBER: US/09/910,174A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US/09/620,461
                                                                                                                                                                                                                                 173 ProGlnProGlnIleLysTrpSer-----
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 584
                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09910174A Patent No. US20020106730A1 GENERAL INFORMATION:
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::: 188 ProAlaValGluAlaProVal	194 GTAGGGATGCTAC		GGCTTGCATGGTTAAGCA		AATCTCGGATGTTCCTT	rileAlaAspProPhePh
188	194	199	242	218	302	236
qa	ò	ΩD	δ	qa	ò	qq

Search completed: July 9, 2003, 12:53:09 Job time : 39 secs hypothetical prote hypothetical prote acetolactate synth transporter, AcrB/ galactose 1-dehydr

pyruvate dehydroge -phosphatidylinos

secretion

general

probable membrane protein

1-phosphatidylinos fibrillin-2 precur

prote

hypothetical

Cpo 61.1

prepilin peptidase hypothetical prote

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Total number

Searched:

Minimum DB s Maximum DB s

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A;Cross-references: EMBL:AL049522; PIDN:CAB40011.1; GSPDB:GN00068; SPDB:SPCC63.07
A;Experimental source: strain 972h-; cosmid c63
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gene forked protei
hypothetical protei
RNA-binding protei
RNA-binding protei
RNA-binding protei
polyprotein (clone
nitrogenase iron-m
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protein kinase C-r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||:::||||||||||||||:::|||
| LysHisGluIleLeuPheSerLysPheGlyIleAsnTyrAsnPheGluProGluIleTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T41508
R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, March 1999
A;Reference number: Z21999
A;Accession: T41508
A;Accession: T41508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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PQ0246
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AB1882
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S24761
T00353
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137451
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A;Introns: 79/2; 179/3; 214/3
                                 1-261 <MUR>
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-MODEL=frame+ n2p.model -DEV=x1p
-Q=CQGD2 11/025TO Spool/USO914191/runat 09072003 112350 12889/app query.fasta_1.775
-Q=CQGD2 11/02FTO Spool/USO914191/runat 09072003 112350 12889/app query.fasta_1.775
-Q=CQGD2 11/02FTO Spool/USO914191/runat 09072003 112350 12889/app query.fasta_1.775
-UNITS=BIR 73 -QFWT=fastan -SUFFIX=rpr -MINMATCH=0.ī -LOOPCL=0 -LOOPEXT=0
-UNITS=Bits -START=1 -END=-1 -MATRIX=blooun62 -TRANS=human40 .cdi -LIST=45
-UNITS=Bits -START=1 -END=-1 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=BITS - NOME=LOCAL
-USER=USO914191 @CGN 1 1 62 @TUNAT -DSPBLOCK=I00 12889 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQÜERY -NEG SCÖRES=0 -WAIT -DSPBLOCK=I00 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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membrane-bound lyt
                                                                               ; Search time 25 Seconds (without alignments) 4599.071 Million cell updates/sec
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                                                                                                                                                      ttggaatagttcttgcttta......ggtgttagtccagattgttg
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                        protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    283224 segs, 96134422 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                               9, 2003, 12:46:18
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S64315
G84731
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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seq length: 2000000000
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genome polyprotein

В.G.

205

169.5 122 94 90 85 83.5 82.5 81.5 81.5

2500

80. 78.

Score

No. Result

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hypothetical protein At2g11580 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84722
R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul S.; Cronin, L.A.; Shen, M.; Won, W. C.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     535 AAGAATGAGATTTTTTTTTTTCAACTTCAACTATAATAATGAGCTGCCGATGTAT 476
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394 LysSerGlyLysAsnLysThrGlnSerGlnAspTyrLeuLysGlyThrGlnThrArgGlu 413
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A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Croser treferences: GB:AE002093; NID:g3831463; PIDN:AAC69945.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g32330
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| ArgMetGlySerSerValPheArgLeuLysVal 277
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A,Residues: 1-457 <STO>
A,Cross-references: GB:;
C,Genetics:
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Best Local Similarity:
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A,Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YGR024c - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein G4041
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revisiae
C;Date: 17-May-1996 #sequence_revision
C;Accession: S64315
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
Bindiecule to the Protein Sequence Database, May 1996
A;Reference number: S64071
A;Accession: S64315
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C.Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C.Accession: G84731
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L., Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                      239 IleLeuHisValSerLeuIleAspAspAspPheTrpThrSerArgProPheLeuGluVal 258
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                                                                                                                    CTGCCAACAGAAATGGAAGGAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTG
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Superfamily: Saccharomyces cerevisiae hypothetical protein YGR024c
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Matches:
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Indels:
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122.00
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Protein TINIS.7 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rocney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Accession: F96524
A;Accession: F96524
                                                                                                                                                                                                                                         362 CTITGICCIGGICCGGGICACIGCCAICITITITICCTICCAITICIGITIGGCAGCTIAAT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AGAGTAAGATACACCCCCCCATCCAT 132
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                                         AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 TTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGAT 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LeuLeuTrp 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE005173; NID: 98778686; PIDN: AAF79694.1; GSPDB: GN00141
                                                                                                                                                         :::|||
MetCys1leSerProHisHisHisHisLeuLeuHisHisHisLeu---
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Matches:
Conservative:
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HisLeuLeuHisLeuLeuProHisHisLeuPro---
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JS-09-914-191-1 (1-598) x S54157 (1-279)
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33.16%
23.68%
7.53%
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A;Molecule type: DNA
A;Residues: 1-343 <STO>
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Best Local Similarity:
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R; Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A.
submitted to the EMBL Data Library, April 1995
A; Bescription: A class of root-hair specific extensins involved in rhizobium/legume inte
A; Reference number: S54155
A; Accession: S54157
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                C;Species: Bombyx mori cytoplasmic polyhedrosis virus strain H C;Species: Bombyx mori cytoplasmic polyhedrosis virus, BmCPV C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 20-Jun-2000 C;Accession: JE0212 R;Hagiwara, K.; Tomita, M.; Kobayashi, J.; Miyajima, S.; Yoshimura, T. Biochem. Biophys. Res. Commun. 247, 549-553, 1998 A;Itle: Nucleotide sequence of Bombyx mori cytoplasmic polyhedrosis virus segment A;Accession: JE0211; MUID:98321164; PMID:9657006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAATGAGATTTTGTTT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAATGGAAGGAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCAC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 TCTGAATTCAACATCAACTATAATAAT-----GAGCTGCCGATGTATAGGAAAGGG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 ACTGTGTTGATATGGCAGAAGGTGGATGAAGTGACAAAAGAAATTAAGCTGCCAACA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 AspMetGlu------ValAlaThrProLysValLeuGluProProThrProLeuPro 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 TGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGC 287
                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-390 <HAG>
A;Cross-references: GB:AB016437; NID:g3395152; PIDN:BAA32043.1; PID:g3395153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            extensin-like protein - cowpea (fragment)
C;Species: Vigna unguiculata (cowpea)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 03-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279
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231 Leupro 232
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Best Local Similarity:
Query Match:
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Query Match:
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Residues: 1-279 <ARS>
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Pred. No.:
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Pred. No.:
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us-09-914-191-1.rpr

Qy 298 GATGAAGACAGCTGACCCTTTTGC	ostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 74-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 nn: AF2172
Qy 274GCTTCA	R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watahabe, A.; Iriguon Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
Oy 250 ATGCAAGCCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAGCATCCCTACCAC 191 :::::	A,Reference number: AB1807; MUID:21595285; PMID:11759840 A,Accession: AF2172 A,Accession: preliminary A,Molecule type: DNA
Oy 190 CCAGGACACTGGTGCGAATGACACACTCAAGTTGGGAGGGA	Airesidues: 1-410 KNUK> Aiross-references: GB:BA000019; PIDN:BAB74632.1; PID:g17132027; GSPDB:GN00179 A:Experimental source: strain PCC 7120 C;Genetics:
OY 130 GGATGGGGGTGTATCTTTAAGCAGAACACCTTGTTTGGGTG 78 :	A,Gene: alr2933 Alignment Scores: 5.1 Length: 410
RESULT 10 JE0211 hypothetical 44k protein - Bombyx mori cytoplasmic polyhedrosis virus strain I C;Species: Bombyx mori cytoplasmic polyhedrosis virus, BmCPV	Score: 80.50 Matches: 44 Percent Similarity: 35.33\$ Conservative: 15 Best Local Similarity: 26.35\$ Mismatches: 44 Query Match: 7.29\$ Indels: 7 DB:
C.;bate: 2.1-Aug-1988 #sequence_revision 21-Aug-1998 #text_change 20-Jun-2000 C;Accession: JED211 R;Hagiwara, K.; Tomita, M.; Kobayashi, J.; Miyajima, S.; Yoshimura, T. Biochem: Biophys. Res. Commun. 247, 549-553, 1998 A;Title: Nucleotide sequence of Bombyx mori cytoplasmic polyhedrosis virus segment 8. A;Reference number: JED211; MUID:98321164; PMID:9657006	US-09-914-191-1 (1-598) x AF2172 (1-410) QY 478 TATAGGAAAGGACTGTTGATATGGCAGAAGGATGATGATGACAAAAGAAATT 419 Db 251 1YrAlaGlydlythrAspTyrProTrpThrSer1leGlyArgGlubeuAlaLysAspGly 270
A;Accession: JE0211 A;Molecule type: mRNA A;Residues: 1-390 <hmg> A;Cross-references: GB:AB016436; NID:g3395150; PIDN:BAA32042.1; PID:g3395151</hmg>	Qy 418 AAGCTGCCAACAGAAATGGAAAGAATGGCAGTGACCCGGACCAGGACAAAG 362 Db 271 LysLeuProleuSerGlyMetThrMetProLysMetIle
Alignment Scores: Pred. No.: 4.49 Length: 390 Score: 81.00 Matches: 27 Percent Similarity: 49.02\$ Conservative. 23	Qy 361 CCAGTGCCCTTGCACTGCGATATCATCGGGGATGCTTTCTGGAAGGAA
Conservative: Mismatches: Indels: Gaps:	Oy 301 CTA
US-09-914-191-1 (1-598) x JE0211 (1-390)	Qy 283 CCTTTTGCGCTTCAGTTCTGGTGTGTGTAACCATGCAA245
Qy 577 GTACAAGCCCAAGGGAGATTACAGGGAACTCTINCAGCAGACAAGAATGAGATTTGTTT 518	Db 313 ProAlaThrGlySerIleAsnValProValThrProGluArgSerIleAlaThrAspLys 332 Qy 244 GCCTCCCACTCCTAGGCTTCTTAGGTGGCTGTAGCATCCTT 196
Qy 517 TCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAAGGG 467	Db 333 SerLeuMetPro-ProGlyAlaLeuAlaLeuValHisThrSerIleProPheProValAl 352 Qy 195ACACCCAGGACACTGGTGC 176
Oy 466 ACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAGAAATTAAGCTGCCAACA 407 ::: :::	
Oy 406 GAAATGGAAGGAAAGATGGCAGTGACCCGGACCAGGACAAAGCAGTGCCCTTGCAC 347	
TCGGGGATGCTTTCTGCAAGGACATCCAGAGATTCTAGATGAAGACAGC	::: 391 yAepArgAlaGlyValThr SULT 12
Oy 286 TGACCC 281	T18319 hypothetical protein L7610.10 - Leishmania major C;Species: Leishmania major C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
RESULT 11 AF2172 membrane-bound lytic transglycosylase A alr2933 [imported] - Nostoc sp. (strain PCC 7126 C;Species: Nostoc sp.	C;Accession: T18319 R;Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.; submitted to the EMBL Data Library, May 1999 A;Reference number: Z18876 A;Accession: T18319

	ent Similarity: 37.86%
Length:	· Internation
Length: 320 Matches: 44 Matches: 52 Indels: 52 Indels: 65 Gaps: 7 TTAAACAGACTAACACCACCCCCAT 128 Indels: 65 Gaps: 7 TTAAACAGACTAACACCACCCCCAT 128 Mismatches: 65 Gaps: 11	1-1 (1-598)
Mismatches: 52 Indels: 7 Indels: 7 1320) TTTAAACAGAGTAAGATACACCACCCCCAT 128	AGGAGCCTGG
TTAAACAGACTAACACCACCCCCAT 128	109 LyshisProTrpAspPr 253 TTAAGCACACCAGAACT
TTTAAACAGAGTAAGATACACCACCCCCAT 128	
ASSISTED CONTROLLED BY THE STREET OF THE STR	313 GTTCCTTCCAGAAAGCK
AsnHisLeuSerLeuCysValPheLeuSerGlyLysAsp 108	
ProSerProProProCrateCrateCrate 155 ProSerProProProSerProProSerLeuHisProSer 128 PACCAGTGTCCTGGGTAGGATGCTACAGCCACTA 215	yProSer
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SGGAGGCATTCCAGAAAGCA 269 SIJANGARGCATCCAGAAACT 269 SIJANGARGCAGACACAGAAAAGCA 329 SISTACAGAATCCTGGATGATCCTTCCAGAAAAGCA 329 SISTACAGAATCTCTGGATGATCCTTCCAGAAAAAAAAAAAA	463 CAGICCCITICCIAIAC
3GGGGGCTTGCATGGTTAAGCACCACAAACT 269 31yArgArgArgSerAlaAlaSerHisLeuAlaGlu 145 31yArgArgCygBArgSerAlaAlaSerHisLeuAlaGlu 145 31yArgArgCygBArgSerAlaAlaSerHisLeuAlaGlu 145 31iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	194 rAla
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rcrrcarcragaarcrcrggaargrrccracaaaagca 329 ii: iii: iiii iii jiii laargGluargargLysLysGlyThrGlyargArgArgasp 165 taargGluargargCrrgGrcc	203
AAGGGCACTGGCTTGCTCCGGGTC 380 AlaCysPheSerPheValleu-SerValalaGluThrTh 185 ATTCTGTTGGCAGCTTAATTCTTTTGTCATCACTCA 440	rg ysaccharide biosynthesiges: Bacillus halodurans
AlaCysPheSerPheVall	01-Dec-2000 #sequence_; sion: H84071
ATTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCA 440	i, H.; Nakasone, K.; Tal Acids Res. 28, 4317-43
ACAGTCCCTTTCC 474 ::: ::: ::: :::	: Complete genome sequer ence number: A83650; MU: sion: H84071 s: preliminary
:: :	ule type: DNA ues: 1-397 <sto></sto>
norhabditis elegans Lon 29-Oct-1999 #text_change 29-Oct-1999 September 1999 rom GB/EMBL/DDBJ	-reterences: GB:AP001518 imental source: strain (ics:
Nornabditis elegans Ion 29-Oct-1999 #text_change 29-Oct-1999 September 1999 rom GB/EMBL/DDBJ	BH3376
September 1999	t Scores: .: Similarity:
rom GB/EMBL/DDBJ	al Similarity: 2 tch:
Le type: DNA	US-09-914-191-1 (1-598) x H840
VID:e1549770; PIDN:CAB55053.1; CESP:Y50E8A.j Db	19 TATAAAAATAGTACTGC ::: 149 TrpLysTyrSerThrGl
λδ	58 CCAAAGGAACCATGTTC
Alignment Scores: 7.8 Length: 225 Db 1	169 ProSerAsnTrpLeuAs

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akaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir. 331, 2000
ence of the alkaliphilic bacterium Bacillus halodurans and NUD:20512582; PMID:11058132
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                                                                                                                                                                                                CTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGAT 312
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AsnHisTyrLeuLysGluLeuPheCysLeuLysGlyValArglle 188
                                                                                                                                                                                                                                                              CATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGG 372
                                                                                                                                                                                                                                                                                                                             TCTTTTTTCCTTCCATTTCTGTTGGCAGCTT-----AA 420
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------AlaAsnLeuGlnPheArgLeuPr 203
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                                                                                                                                   --- GGGCTTGCATGG
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Matches:
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Oy 274 GCTTCAGTTCTGGTGGTTAACCATGCAAGCCCTCCCAGGGCTCCTTGCCTT 215 Db 595ArgLysLeuArgGluLeuAlaMetLeuAlaLysProGlnSerAsnValProAlaAla 613 Oy 214 AGGTGGCTGTAGCATCCTACCAGGACACTGGTGGAATGACACACTCAAGTTGG 155 1	Qy 97 AGAACACCTTGTTTGCGGTGTTGGAAC	Qy 58 GCAGAAGTGCTTTTTTTTAATCGCAGTACTATTT 23 ::	Search completed: July 9, 2003, 12:51:24 Job time : 30 secs									
Qy 118 ACCACCCCCATCCATCCTTCCTTCCTTCCTTCCTTCCTT	Oy 226 CCCTGGGAGGTGGGAGGCTTGCATGGTTAAGCACACAGAACTGAAGGGCAAAAGG 282	Oy 283 GTCAGC 288 :: Db 264 ValAsn 265	T18274 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 3 - slime mold (Dictyostellum discoideum) C; Species: Dictyostellum discoideum C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T18274 R; Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A. Mol. Cell. Biol. 15, 5645-5656, 1995 A; Title: A phosphatidylinositol (PI) kinase gene family in Dictyostellum discoideum: Biol. 15, 1000 1000	A; Accession: T18274 A; Accession: T18274 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Rosiduss: 1.1585 < ZHO> A; Cross_references: EMBL: U23478; NID: g733523; PID: g733524; PIDN: AAA85723.1 C; Genetics: A; Gene: PICS C; Keywords: phosphotransferase	Alignment Scores: Pred. No.: Score: Score: Score: Percent Similarity: 38.29% Query Match: Alignment Scores: 10.0% Description of the state	-09-914-191-1 (1-598) x T18274 (1-1585)	Qy 571 GCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAAAGAATGAGATTTGTTTTGT	Oy 514GAA 512 Db 518 ArgTrpCysAsnLysAspValValPheAspGlnAspThrProLeuGlyHisLeuIleGln 537 '	Qy 511 TTCAACATCAATAATAATGAGCTGCCGATGTATAGGAAAGGGACTGTTGATATGG 452 ::: ::	Qy 451 CAGAAGGTGGATGAAGAAAATAAAGCTGCCAACAGAAAATGAAGGAAAA 392 ::::: ::: ::: 	Oy 391 AAGATGCCAGTGACCCGGACCAGGCCAGTGCCCTTGCACTGCGATATCATCGGG 332 1:: ::	Qy 331 GATGCTTTCTGGAAGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGC 275 :::

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homo sapien gallus gall

Minimum DB Maximum DB M

Searched:

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gallus gall

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Run on:

Sequence:

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288c;
MEDLINE-97435481; PubMed-9290212;
Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
"Sequence analygis of 203 kilobases from Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGIG YEAST STANDARD; PRT; 237 AA.
P53215;
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 27.8 kDa protein in VMA7-RPS25A intergenic region.
                                                     0911j4 pp6662 pp6662 pp6662 pp6662 pp7696 pp2886 pp29846 pp21256 pp21256 pp61259 pp61256 pp61256 pp61256 pp61256 pp6139 pp6139 pp61393 pp61393
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YPRO OWEPU
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Query Match:
                  NCBI_TaxID=4932;
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             version 5.1.6
- 2003 Compugen Ltd.
                                                                                       - protein search, using frame_plus_n2p model
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MYOC MOUSE
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CLN2 RAT
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DTNB MOUSE
DTNB MOUSE
DINA HUMAN
SLDA BACAN
SLDA BACAN
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                  GenCore (c) 1993
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Match Length
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Database

No No Result

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us-09-914-191-1.rsp

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Alternative splicing DOMAIN
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                                                                             GGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAAT 530
                                                                                                     470
                                                                                                                                                                                  ENP2 RAT STANDARD; PRT; 495 AA.

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation)
16-
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COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.

COPACTOR: REQUIRES CALCIUM AND MAGNESIUM.

SUBCELLULAR LOCATION: Integral membrane protein (Potential).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, VAS DEFERENS,
KIDNEY, SKELETAL MUSCLE, THYMUS, LUNG AND SPLEEN. WEAK EXPRESSION
                                                                                                                                                             GAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain Res. Mol. Brain Res. 73:85-92 (1999).
--- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER NUCLECTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES ADP ONLY TO A MARGINAL EXTENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
STRAIN=Sprague-Dawley, TISSUE=Brain;
MEDLINE=98031057; PubMed=9364474;
Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
"An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: BY FSH IN SERTOLI CELLS BUT NOT IN PERITUBULAR CELLS; BY CAMP IN BOTH TYPE OF CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vlajkovic S.M., Housley G.D., Greenwood D., Thorne P.R.; "Evidence for alternative splicing of ecto-ATPase associated with termination of purinergic transmission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: HAS PROBABLY DISULFIDE BONDS.
SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=Sprague-Dawley; TISSUE=Sertoli cells;
MEDLINE=21121474; PubMed=11229804;
Lu Q., Porter L.D., Cui X., Sanborn B.M.;
"Ect-ATPase mRNA is regulated by FSH in Sertoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 379-495 FROM N.A. (ISOFORM 2)
STRAIN=Wistar; TISSUE=Cochlea;
MEDLINE=20050856; Pubmed=10581401;
Gaps:
                                US-09-914-191-1 (1-598) x YG1G YEAST (1-237)
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GlySerLeuVal 215
                                                                                                                                                                                                                                               GGGACTGTGTTG 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheTyrTyr-----ThrValAspPheLeu------ThrThrValMetGlyLeuPro 362
                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 LeuleuAlaSerAlaLeuGlnileHisArgPheHisProCysTrpProLysGlyTyrSer 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 ThrGinValLeuLeuGlnGluValTyrGlnSerPro-------CysThrMetGly 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 GCGCAAAAGGGTCAGCTGTCTTCATCT----AGAATCTCTGGATGTTCCTTCCAGAAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  507 TTGAATTCAGAAAACAAAATCTCATTCTTGTCTGCTGNAAGAGTTCCCTGTAATCTCCCT 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 TCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTACAGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 GlnArgProArgAlaPheAsnGlySerAlaIleValSerLeuSerGlyThrSerAsnAla
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                                                                                                                                                                                                                                                            Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
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A -> T (IN REF. 2).
L -> F (IN REF. 2).
; 237B999FIBEBBBEOO CRC64;
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411
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Matches:
Conservative:
Mismatches:
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T -> A (IN REF.
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dified and this statement is not removities requires a license agreement (send an email to license@isb-sib.ch)
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                                                                                                EMBL; Y11835; CAA72533.1;
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363 ValGlyThrLeuLysGlnLeuGlu-----GluAlaThrGluIleThrCysAsnGlnThr 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Relischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackehbush J., Schriml L., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Loons P., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Loons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshing K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshing L., Wanshing K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshing L., Wanshing L., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                     mouse gene with homology to ecto-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES ADP ONLY TO A MARGINAL EXTENT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate,
COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
SUBCELLULAR: LOCATION: Integral membrane protein (Potential)
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   re 403:665-650(2001).
FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                  ENP2 MOUSE STANDARD; PRT; 495 AA.
055026; 035928; Q9DCR9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ecconucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
(NTPDase2) (Ecto-ATPase) (CD39 antigen-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of ecto-ATPase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: HAS PROBABLY DISULFIDE BONDS.
SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING. INDUCTION: BY DIOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao L., Dong L., Whitlock J.P. Jr.;
"A novel response to dioxin. Induction
                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and mapping of a human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 273:15358-15365(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97419269; PubMed=9271669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Hepatoma; MEDLINE=9624117; MEDLINE=98288117;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                     Chadwick B.P., Frischauf A.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                ATPase genes.";
Mamm. Genome 8:668-672(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001)
                                                                                                                                                                                                                                            Wus musculus (Mouse)
                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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Trp 381
                              TGG 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 CAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 ACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCA 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 AsnAlaAlaLeuCysArgAspLeuValSerGlyLeuPheAsnileSerSerCysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 GlnArgLeuLeuAlaSerAlaLeuGlnIleHisArgPheHisProCysTrpProLysGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 ACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT----AGAATCTCTGGATGTTCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
LIS -> MAG (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
T -> A (IN REF. 3).
S -> R (IN REF. 3).
T -> A (IN REF. 3).
T -> A (IN REF. 3).
W, CC0811C5D79CA4C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                            PROSITE: PS01238; GDA1_CD39 NTPASE; 1.
Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ValPheGlnProProValAla---GlyAsnPheIleAlaPhe
                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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Mismatches:
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Matches:
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                                                                                                                                                                           MGD; MGI:1096863; Entpd2.
InterPro; IPR000407; GDA1 CD39 NTPase.
Pfam; PF01150; GDA1 CD39; 1.
                                                                                                                                        EMBL; AF042811; AAC24347.1; -. EMBL; AK002553; BAB22182.1; -.
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                                                                                                                           EMBL; U91511; AAB81014.1; -.
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4 62
4 83
4 95
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132
495
                                                                                                                                                                                                                                                                       Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437
495 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity:
                                                                                                                                                                                                                                                                                                                                          463
                                                                                                                                                                                                                                                                                                                                                                              64
129
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133
133
400
414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
VARSPLIC
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No
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SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: UBIQUITOUS.
PTH: PHOSPHORYLATED BY AKT1.
DISBASE: INVOLVED IN A T(6;11) (Q21;Q23) CHROMOSOMAL TRANSLOCATION
IN SECONDARY ACUTE LEUKEMIA THAT INVOLVES FOXO3A AND MLL.
SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
DATABASE: NAME-ARIAS Genet. Cytogenet. Oncol. Haematol.;
WWW*.http://www.infoblogen.fr/services/chromcancer/Genes/AF6q211D125.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                     88 LeuProSerLysLeuSerGluGluLysTyrLysSerGlnLeuGluGlyArgSerLeulle 107
                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Forkhead box protein O3A (Forkhead in rhabdomyosarcoma-like 1) (AF6q21
                                                                                                                                                                                                          -------AAAGAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAAAGATGGCA
                                                                                                                                                 68 LeuAlaProTyrIleLysAsnHisLeuValAlaSerAsnAspLysGluValPheAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillion J., Le Coniat M., Jonveaux P., Berger R., Bernard O.A.;
"AF6G21, a novel partner of the MLL gene in t(6;11) (q21;q23), defines
a forkhead transcriptional factor subfamily.";
Blood 90:3714-3719(1997).
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR THAT MAY TRIGGER
APOPTOSIS BY INDUCING THE EXPRESSION OF GENES THAT ARE CRITICAL
                                                                                                      --GATGAAGTGATGACA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98140118; PubMed=9479491; Anderson M.J., Viars C.S., Czekay S., Cavenee W.K., Arden K.C.; "Cloning and characterization of three human forkhead genes that comprise an FKHR-like gene subfamily."; Genomics 47:187-199(1998).
                                                                                                                                                                                                                                                                                                              GTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGG-
CTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAGAAGGTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               331 GATGCTTTCTGGAAGGAACAT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 GlySerAlaTrpLysGluTyr 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-383 FROM N.A.
MEDLINE=98008138; PubMed=9345057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FXO3 HUMAN STANDARD; 0435Z4; 015171; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequing-15-UN-2002 (Rel. 41, Last annotations)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR CELL DEATH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOXO3A OR FKHRL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Muscle;
187
                                                                                                                                                                                                          427
                                                                                                      442
                                                                                                                                                                                                                                                                                                              382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FXO3_HUMAN
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  GGACTAACACCCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGGACAAGAAT 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529 GAGATTTTGTTT--------TCTGAATTCAACATCAACTATAATAATGAG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||::: |||::: |||:::|||:::||| GlylleLeuProLeulleAlaLysGlyLysValArgAspIleTyrAlaValAspGluAsn
                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoribosylamidoimidazole-succinocarboxamide synthase (EC 6.3.2.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 263:159-169(2001).
-!- CATALYTIC ACTIVITY: ATP + 5-amino-1-(5-phospho-D-
ilbosyllimidazole-4-carboxylate + L-aspartate = ADP + phosphate
($\sigma^2 - 2 - 15 - amino-1-(5-phospho-D-ribosyl) imidazole-4-
carboxamido]succinate.
-!- PATHWAY: De novo purine biosynthesis; seventh step.
-!- SIMILARITY: BELONGS TO THE SAICAR SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21125227; PubMed=11223254;
Lin Cereghino G.P., Lin Cereghino J., Sunga A.J., Johnson M.A.,
Lim M., Gleeson M.A.G., Cregg J.M.;
"New selectable marker/auxotrophic host strain combinations for
molecular genetic manipulation of Pichia pastoris.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34101 MW; 584073DA712262C9 CRC64;
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23
37
38
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Matches:
Conservative:
Mismatches:
Indels:
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Pfam; PF01259; SAICAR synt; 1.
ProDom; PD003043; SAICAR synt; 1.
TIGRFAMS, TIGR00081; purč; 1.
PROSITE; PS01057; SAICAR SYNTHETASE 1; 1.
PROSITE; PS01058; SAICAR_SYNTHETASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-914-191-1 (1-598) x PUR7_PICPA (1-304)
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                   (Rel. 41, Created)
(Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF321096; AAK06766.1; -
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80.00
40.94%
22.83%
7.24%
                                                                        561 CTCCCTTGGGCT 572
                                                                                                                            379 GlnThrrrphia 382
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pichia pastoris (Yeast).
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4922;
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                                                                                                                                                                                                                               PUR7 PICPA
Q9C1J4;
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                                                                                                                                                                   The State of the s
                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FALSE NEG.
FALSE NEG.
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PS00650; G PROTEIN RECEP F2 2;
PS50227; G PROTEIN RECEP F2 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB011529; BAA88687.1; --
HSSP; P00740; IEDM.
InterPro; IPR001551; Cadherin.
InterPro; IPR001561; Cadherin.
InterPro; IPR001561; EGF-like.
InterPro; IPR00181; EGF-G.
InterPro; IPR00181; EGF-G.
InterPro; IPR001438; EGF-II.
InterPro; IPR001439; EGF-II.
InterPro; IPR001439; EGF-II.
InterPro; IPR001439; Hormi receptor.
InterPro; IPR001791; Laminin EGF.
InterPro; IPR001791; Laminin GF.
InterPro; IPR001791; Laminin GF.
Ffam; PF00023; PRD_Cys_rich.
Pfam; PF00023; PRD_Cys_rich.
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SWART; SW00179; EGF CA; 1.
SWART; SW00019; EGF Ilke; 6.
SWART; SW00303; GPS; 11.
SWART; SW00009; HOTMR; 1.
SWART; SW00009; HOTMR; 1.
SWART; SW00289; LamiG; 2.
PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS00232; CADHERIN 1; 3.
PROSITE; PS00269; CADHERIN 2; 4.
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LAM G DOMAIN; 2.
EGF_1; 6.
EGF_2; 4.
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GPCRSECRETIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02793; HRM; 1.
Pfam; PF00054; laminin G; 1.
PRINTS; PR00205; CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGFBLOOD
                                                                                                                                                       SEQUENCE FROM N.A
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PRINTS; PR00010; E
PRINTS; PR00011; E
PRINTS; PR00249; G
                                                                                                      NCBI_TaxID=10116;
          CELSR2 OR MEGF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00008;
Pfam; PF01825;
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       CAAGGIGITICIGCITAAACAGAGATACACCACCCCCATCCATCCTTCCTTCCCTG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerValSerAsnMetGlyLeuSerGluSerSerLeuGlySerAlaLysHisGlnGln 572
                                                                                                                                                                                                     -> AWQPHVNAAVNSWRGRTSVHAPILTPAQSVAACRPSW QV (IN REF. 3).
PMLYSSSASLSPSVSKP -> AHALQHVSQPVTFSKQA (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 AGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGCTTGCATGGTTAAGCACACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 TTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AWGNLSYA -> WGKPUYS (IN REF. 3).
PDGGKGGKA -> LWGEERKT (IN REF. 3).
S -> T (IN REF. 3).
MISSING (IN REF. 3).
PGSSPTGRSSDELDAWTDFRSRTNSNASTVSGRLSPIMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GINSETProVal-SerGINSETMetGINThrLeuSerAspSerLeuSerGlySer 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 GCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTCA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 2 (Multiple epidermal growth factor-like domains 3) (Fragment).
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E5B4E830665A9982 CRC64;
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L; BCC21224; AAH30227.1; -...
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C; AJ001590; CAA04861.1; -...
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PROSITE; PS50261; G PROTEIN RECEP F2 4; 1.

PROSITE; PS01248; LAMININ_TYPE_EGF; I.

G-protein coupled receptor; Transmembrane; Glycoprotein;
EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
Developmental protein; Hydroxylation.

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LAMININ G-LIKE 2.
EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
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CADHERIN 4.
BGF-LIKE 1, CALCIUM-BINDING.
BGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
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10-OCT-2001 (Rel. 40, Last annotation update)
11-OCT-2001 (Rel. 40, Last annotation update)
12-OCT-2001 (Rel. 40, Last annotation update)
13-OCT-2001 (Rel. 40, Last annotation update)
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14-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 34, Last annotation update)
16-OCT-2001 (Rel. 34, Last annotation update)
16-OCT-2001 (Rel. 34, Last annotation update)
17-OCT-2001 (Rel. 34, Last annotation update)
18-OCT-2001 (Rel. 34, Last annotation update)
18-OCT-2001 (Rel. 34, Last annotation update)
19-OCT-2001 (Rel. 34, Last annotation u
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570 AsnLeuLeuValGlyGlyPheLysCysAspCysProSerGlyAspPhe
N-LINKED (GLCNAC. ..) (POT)
N-LINKED (GLCNAC. ..) (POT)
N-LINKED (GLCNAC. ..) (POT)
N-LINKED (GLCNAC. ..) (POT)
MW; 6EA898C1BA655ECA CRC64;
                                                                                                                                                                                                                                                                                                                            2144
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Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 ATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTC
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Mismatches:
Indels:
Gaps:
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Matches:
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STRAIN=AX3;
MEDLINE=96009592; PubMed=7565716;
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AA; 233480 M
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79.50
34.02$
22.16$
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391 AAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGG 332
                                                                                                                                                                                                                     GATGCTTTCTGGAAGAACAT---CCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGC 275
                                                                                                                                                                                                                                                                                                                          ---ArgLysLeuArgGluLeuAlaMetLeuAlaLysProGlnSerAsnValProAlaAla 613
                                                                                                                                                                                                                                                                                                                                                               AGGTGGCTGTAGCATCCCTACCACCAGGACACTGGTGCGAATGACACCAACTCAAGTTGG 155
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                                                                                                                                                                                                                                                                                           GCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCCACCTCCCAGGGCTCCTTGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                             Blake D.J., Nawrotzki R., Loh N.Y., Gorecki D.C., Davies K.E., "Beta-dystrobrevin, a member of the dystrophin-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GCAGAAGTGCTT------TTTTTTTAATCGCAGTACTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=99018217; PubMed=9799833;
MEDLINE=100 N.Y., Ambrose H.J., Guay-Woodford L.M., Dasgupta S.,
Nawrotzki R.A., Blake D.J., pavies K.E.;
"Genomic organization and refined mapping of the mouse beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98200066; PubMed=954099;
MEDLINE=101050 V.N.G., Belsito A., Sampaolo S., Quaderi
Rossi E., Di Iorio G., Ballabio A., Franco B.;
"Identification and characterization of a novel member of t
                                                                                                                                                                                                                                         (MDTN-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 AGAACACCTTGTTTGCGGTGTTGGAAC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.";
Proc. Natl. Acad. Sci. U.S.A. 95:241-246(1998)
                                                                                                                                                                                572 SerLeuGluIleAsnAsnGlyArg------
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MEDLINE=98081858; PubMed=9419360;
Blake D.J., Nawrotzki R., Loh N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dystrobrevin gene.";
Mamm. Genome 9:857-862(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dystrobrevin gene family.";
FEBS Lett. 425:7-13(1998).
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                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
"A phosphatidylinositol (PI) kinase gene family in Dictyostellium discoideum: biological roles of putative mammalian pil0 and yeast vps34p PI 3-kinase homologs during growth and development.";
Mol. Cell. Biol. 15:5645-5656(1995)
-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP 1-phosphatidyl-1D-myo-inositol 3-phosphate.
-!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
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Matches:
Conservative:
Mismatches:
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PROSITE; PS00916; PI3 4 KINASE 2; 1.
PROSITE; PS50290; PI3 4 KINASE 3; 1.
Transferase; Kinase; Multigene family; Repeat.
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InterPro; IPR002420; PI3K_C2.
InterPro; IPR00341; PI3K_ras_bind.
InterPro; IPR001263; PI3Ka.
InterPro; IPR000403; PI3Ka.
InterPro; IPR000403; PI3 PI4 kinase.
Pfam; PF00454; PI3 PI4 kinase; I.
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Pfam; PF00794; PI3K_rbd; 1.
SMART; SM00142; PI3K_C2; 1.
SMART; SM00145; PI3K_rbd; 1.
SMART; SM00145; PI3Ka; 1.
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SEQUENCE
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                                                                       A Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H.. Baldarelli R., Barsh G., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whithaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:585-590 (2001).

-1- SUBUNIT: INTERACTS WITH DYSTROPHIN SHORT FORM DP71 AND SYNTROPHIN.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- ATTERNATIVE PRODUCTS: AT LEAST 2 ISOPORMS; 1 (SHOWN HERE) AND 2;
ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN BRAIN, KIDNEY, LIVER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUNG. IN BRAIN EXPRESSED IN NEURONS OF THE CORTEX AND HIPPOCAMPUS.
-!- DOMAIN: THE COILED-COIL DOMAIN MAY MEDIATE THE INTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE DYSTROPHIN FAMILY. DYSTROBREVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Machine | Mach
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  (ISOFORM 2)
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JOINED.
JOINED.
SEQUENCE OF 590-608 FROM N.A. (ISOF
STRAIN=C57BL/6J; TISSUE=Stomach;
MEDLINE=21085660; PubMed=11217851;
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CAA09038.1;
CAA09038.1;
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AJ010204; CAA09038.1;
AJ010205; CAA09038.1;
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MEDLINE=96254978; PubMed=8845841;
Sadoulet-Puccio H.M., Khurana T.S., Cohen J.B., Kunkel L.M.;
"Cloning and characterization of the human homologue of a dystrophin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Q9Y4Ū8; Q13498; O15333; Q13499; Q13199; Q13500; O15332; O75697;
Q13197; Q13198;
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           K -> KEEEQKQA (IN ISOFORM 2).
AEAEEQ -> EVTPVS (IN ISOFORM 2)
MISSING (IN ISOFORM 2).
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                                                     P -> L (IN REF. 2 AND 3).
S -> F (IN REF. 2 AND 3).
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Conservative:
Mismatches:
Indels:
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16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Dystrobrevin alpha (Dystrobrevin-alpha)
                                                                                                                             Length:
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521 CC
518 K
608 AR
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412 P
462 P
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Genew; HGNC:3057; DTNA.
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           ACETYLCHOLINE RECEPPORS.

1. SUBGINIT: INTERACTS WITH DYSTROPHIN UTROPHIN AND SYNTROPHIN.

1. SUBGINIT: INTERACTS WITH DYSTROPHIN. UTROPHIN AND SYNTROPHIN.

2. SUBGINIT: INTERACTS WITH DYSTROPHIN.

3. SUBGELLULAR LOCATION: CYLOPISMIC.

4. SUBGELLULAR LOCATION: CYLOPISMIC.

5. PATTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS; 1/DTN-1 (SHOWN HERE),

5. OYSTROBREVIN-3/DYSTROBREVIN-BETA.

5. OYSTROBREVIN-3/DYSTROBREVIN-DELTA AND 8/DYSTROBREVIN-ZETA; ARE

PRODUCED BY ALTERNATIVE SPLICING.

7. TISSUE SPECIFICITY: HIGHLY EXPRESSED IN REALN. SKELETAL AND

CARDIAC MUSCLES, AND EXPRESSED AT LOWER LEVELS IN LUNG, LIVER AND

CARDIAC MUSCLES, AND EXPRESSED AT LOWER LEVELS IN LUNG, LIVER AND

CARDIAC MUSCLES. IS NOT EXPRESSED IN CARDIAC MUSCLE. ISOFORMS 7

CARDIAC MUSCLED-COIL DOMAIN MEDIATE THE INTERACTION WITH

DYSTROPHIN AND UTROPHIN (BY SIMILARITY).

CONSTRUCTION OF DIVINIARITY).

CHESENT IN THE C-TERMINUS BY SIMILARITY).

CHESENT IN THE C-TERMINUS BY SIMILARITY.

CHESENT IN THE C-TERMINUS BY SIMILARITY.
                                                                                                                                                                MEDLINE=98359056; PubMed=9701558;
Nawrotzki R., Loh N.Y., Ruegg M.A., Davies K.E., Blake D.J.;
Nawrotzki R., Loh A.Y., Ruegg M.A., Davies K.E., Blake D.J.;
"Characterisation of alpha-dyptrobrevin in muscle.";
J. Cell Sci 111:2595-2605 (1998)
-!- FUNCTION: MAY BE INVOLVED IN THE FORMATION AND STABILITY OF
SYNAPSES AS WELL AS BEING INVOLVED IN THE CLUSTERING OF NICOTINIC
related phosphoprotein found at the Torpedo electric organ post-
                                    [2]
SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 7).
MEDILINE=20197320; PubMed=1073523;
Sadoulet-Puccio H.M., Feener C.A., Schaid D.J., Thibodeau S.N.,
Michels V.V., Kunkel L.M.;
"The genomic organization of human dystrobrevin.";
Neurogenetics 1:37-42(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
              synaptic membrane.";
Hum. Mol. Genet. 5:489-496(1996).
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TISSUE=Fetal brain;
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U26742; AAC50424
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MISSING (IN ISOFORM 3, ISOFORM 4, ISOFORM
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MISSING (IN ISOFORM 6 AND ISOFORM 8)
MISSING (IN ISOFORM 4, ISOFORM 6 AND
MISSING (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IN ISOFORM 2, ISOFORM 5 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AND ISOFORM 8).
H -> Q (IN REF. 1 AND 3).
E -> K (IN REF. 3).
EVL -> AVF (IN REF. 1 AND 3).
E -> K (IN REF. 1, AAC50431).
AGSP -> SCTH (IN REF. 1; AAC50429).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPKDSEVE -> DGAFGGCV (IN ISOFORM 7).
MISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 6).
TQGAGSPRSEPSHIS -> EEELKQGVSYVPYCRS
ISOFORM 3, ISOFORM 4, ISOFORM 5 AND
ISOFORM 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNTROPHIN-BINDING REGION
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T -> S (IN REF. 1).
T -> S (IN REF. 1).
CO57EA485723C022 CRC64;
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23
55
73
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PROSITE; PS01357; ZF ZZ, 1.
PROSITE; PS50135; ZF ZZ, 2, 1.
Synapse; Coiled coil; Zinc-finger; Phosphorylation;
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Conservative:
Mismatches:
Indels:
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83933 MW, T
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AAB58542.1;
AAB58542.1;
AAB58542.1;
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                                      AAB58542.1;
AAB58542.1;
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7.06%
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AAB58541.1
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ZN FING 237 284
DOMAIN 400 450
DOMAIN 461 556
VARSPLIC 335 337
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Usage

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is not removed.
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                                                                                         wall; S-layer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536 ThrThrAspGlnTyrGlyAsp----
                                                                                                               862 S-1
76 SLJ
136 SLJ
197 SLJ
91362 MW;
                                                 EMBL; X99724; CAA68063.1; -.
InterPro; IPR001119; SLH.
Pfam; PF00395; SLH; 3.
Signal; Repeat; Cell wall; S-
SIGNAL
 modified and this statement
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78.00
39.55%
24.86%
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SEQUENCE
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                                                                                                                                                         395
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                                                   GCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAATGAGATTTTGTTTTCTGAA 512
                                                                         135 AlaLeuAlaThrLeuCysGlyGlyLysIleMetAspLysLeuArgTyrIlePheSerMet 154
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                                                                                                                                                                                                                                                                                                                                                                                               218 ProproGln-----CysLeuValTrpLeuProLeuLeuHisArgLeuAlaAsnValGlu 235
                                                                                                                                                                                                                                                                                                                                                                                                                           ------PheArgTyrArgCysGln 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGGAAGGGATGGAGGTGTGTATCTTACTCTGTTTAAGCAGAACACCTTGTTTG .83
                                                                                                    511 TTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGG
                                                                                                                                                         451 CAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAGCTGCCAACAGAA---ATGGAAGGA
                                                                                                                                                                                                                           -----GlyPheLeuAsp
                                                                                                                                                                                                                                                                                                                                            -----ThrLeuMetSerAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AsnValPheHisProValGluCysSerTyrCysHisSerGluSerMetMetGly-----
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Microbiol. 23:1147-1155(1997).

FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAI THE SURFACE OF BACTERIA.

SUBCELLULAR LOCATION: Cell wall.

SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sterne / 9131;
MEDLINE=97260111; PubMed=9106206;
Mesnage S., Tosi-Couture E., Mock M., Gounon P., Fouet A.;
"Molecular characterization of the Bacillus anthracis main S-layer component: evidence that it is the major cell-associated antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus anthracis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 GlnCysHisAsn-TyrGlnLeuCysGlnAspCysPheTrp 272
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             862 AA
Gaps:
                       US-09-914-191-1 (1-598) x DTNA_HUMAN (1-743)
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                                                                                                                             155 IleSer-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 AGCTGACCCTTTTGCGCTTCAGTTCTGGTGCTTAACCATGCAAGCCCTCCCACCTCCC 230
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-----ProPheGlyAlaAsn-----ThrAlaAlaIleLysGluValLeuProLys-Th
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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S-LAYER PROTEIN EAL.
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                                                                                                                                        MEDLINE=94140368; PubMed=8307578;
Li X., Pereira L., Zhang H., Sanguineti C., Ramirez F., Bonadio J.,
Li X., Pereira L., Zhang H., Sanguineti C., Ramirez F., Bonadio J.,
"Fibrillin genes map to regions of conserved mouse/human synteny on
mouse chromosomes 2 and 18 ";
Genomics 18:667-672(1993)
-:- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
THAT BINDS CALCIUM. FIBRILLIAN-LONTANING MICROFIBRILS
ICONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
-:- SIMILARITY: CONTAINS 7 TGF-LIKE DOMAINS.
-:- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=95263670; PubMed=7744963;
Zhang H., Hu W., Ramirez F.;
"Developmental expression of fibrillin genes suggests heterogeneity of extracellular microfibrils.";
"Cell Biol. 129:1165-1176(1995).
"Ronadio J.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                            Yu W., Gibbs R.A.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-! SUBUNIT: INTERACTS WITH DYSTROPHIN SHORT FORM DP71 AND SYNTROPHIN.
-! SUBCELLULAR LOCATION: CYCOPIBEMIC.
-!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; 1/DTN-B1 (SHOWN HERE),
2/DYSTROPHIN-ASSOCIATED PROTEIN A0, 3/DTN-B2 AND 4; ARE PRODUCED
BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, KIDNEY AND
PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DOMAIN: THE COLLED-COLL DOMAIN MAY MEDIATE THE INTERACTION WITH DYSTROPHIN.
-!- SIMILARITY: BELONGS TO THE DYSTROPHIN FAMILY. DYSTROBREVIN
                                                                             Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                             TISSUE=Skeletal muscle; MEDLITE=98200066; PubMed=9540997; MEDLITE=98200066; PubMed=9540997; MEDLITE=98200066; PubMed=9540997; MEDLITE-98200066; PubMed=9820006; Medsi E., Di Iorio G., Ballabio A., Franco B.; Midentification and characterization of a novel member of the EBS Lott. 425:7-13(1998).
                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=89808946; PubMed=9395493;
Peters M.F., O'Brien K.F., Sadoulet-Puccio H.M., Kunkel L.M.
Adams M.E., Froehner S.C.;
"Beta-dystrobrevin, a new member of the dystrophin family.
Identification, cloning, and protein associations.";
J. Biol. Chem. 272:31561-3156(1997).
        060941; 043782; 060881; 075538; 09UE15; 09UE16; Q9UE14; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-UNN-2002 (Rel. 41, Last annotation update) Dystrobrevin beta (Beta-dystrobrevin) (DTN-B).
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SYNTROPHIN-BINDING REGION.
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EMBL, Y12712, CAA75733.1; --
EMBL, Y15718, CAA75733.1; --
EMBL, Y15719, CAA75734.1; --
EMBL, Y15720, CAA75735.1; --
EMBL, Y15720, CAA75735.1; --
EMBL, AF670567; AAC28643.1; --
Genew, HGNC:3058, DTNB.
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MIM; 602415;
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RP SEQUENCE FROM N.A., AN STAIN SMILL 102; RX MEDLINE=89345117; PubM Sperka S., Zehelein E. R. "Complete nucleotide sR dehydrogenase gene."; R. Nucleic Acids Res. 17; C! - CATALYTIC ACTIVITY	+ NAL -!- PATHW -!- SUBUM -!- SUBUM -!- SUBUM -!- SUBUM This SWIE between the Eurog		DR PIR; S04853; S04853. DR INTERPO; IPR000683; GD INTERPO; IPR004104; GD P Pfam; PF01408; GFO IDH DR Pfam; PF02894; GFO IDH KW Oxidoreductase; NAĎ; GS SEQUENCE 304 AA; 33	Alignment Scores: Pred. No.: Score: Percent Similarity: 39. Best Local Similarity: 20. Ouerv Match:	91-1 (1-598) 10 TTCTTGCTTT	70 70 93	Db 113 SerProcysIleA Qy 190 GGTGGTAGGGATG Db 124 AlaAlaArgAsp. Qy 250 TGGTTAAGCACC	Db 128 TrpLeualaThra Qy 310 GATGTTCTTCCA Db 138 GlnileAspTrpL Qy 370 TGGTCCGGGTCAC Db 157 nProGly-Le Qy 430 TCATCATTCATC Db 175 Qy 490 CATTATAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCC 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAATAGTACTGCGATTAAAAAAAAAGCACTTCTGCCAAAGGAACCA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IY: D-galactose + NAD(+) = D-galactono-1,4-lactone
                                  DMed=2503815;
E., Fiedler S., Fischer S., Sommer R., Buckel P.;
sequence of Pseudomonas fluorescens D-galactose
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DH MGCA; 1.
DH-MGCA_C; 1.
Galactose metabolism.
33049 MW; D842A776DC67A3B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGTTGAATTCAGAAACAAAATCTCA 530
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335
58
58
6
                                                                                                                                                                TEP IN D-GALACTOSE CATABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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Gaps:
ND SEQUENCE OF 1-40.
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                                                                                                                                                                                                                                                                                                                                                       icense@isb-sib.ch)
                                                                                                                                                                                   ER.
TION: Cytoplasmic.
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                                                                                                            7:5402-5402 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                        GFO_IDH_MocA.
GFO_IDH_MocA_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

STRAIN-BALB/C; TISSUE-Skeletal muscle;

MEDLINE-99430858; PubMed-9675094;

A Takahashi H., Noda S., Immanura Y., Nagasawa A., Kubota R., Mashima Y.,

Kudoh J., Oguchi Y., Shimizu N.;

"Mouse myoorlin (Myoc) gene expression in ocular tissues.";

"Mouse myoorlin (Myoc) gene expression in ocular tissues.";

"HE TRABECULAR MESHWORK.

-1- FUNCTION: MAY PARTICIPATE IN THE OBSTRUCTION OF FLUID OUTFLOW IN

THE TRABECULAR MESHWORK.

-1- FUNCTION: MAY PARTICIPATE IN THE OBSTRUCTION OF FLUID OUTFLOW IN

ROOTLET AND BASAL BODY OF THE CONNECTING CILIUM OF PHOTORECEPTOR

CELLS. AND IN THE ROUGH ENNOPLASMIC RESTCULUM. ALSO SECRETED.

-1- TISSUE SPECIFICITY: EXPRESSED IN CILIARY BODY, IRIS, RETINA,

TRABECULAR NETWORK AND SCLERA BUT NOT IN LENS OR CORNEA. ALSO

EXPRESSED STRONGLY IN SKELETAL MUSCLE AND WEAKLY IN HEART, BRAIN,

TESTIS, LIVER, KIDDEY, THYROID AND BEDIDIDWHIS. NO EXPRESSION

DETECTED IN EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLYMORPHISM: VARIANT ALA-164 IS FOUND IN STRAIN BALB/CJ WHICH HAS A LOW INTRAOCULAR PRESSURE. VARIANT THR.164 IS FOUND IN STRAINS C3H/HEJ AND C57BL/GJ, TWO STRAINS WHICH HAVE A RELATIVELY HIGH INTRAOCULAR PRESSURE. SIMILARITY: BELONGS TO THE OLFACTOMEDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98217378; PubMed=9548973; Fingert J.H., Ying L., Swiderski R.E., Nystuen A.M., Arbour N.C., Alward W.L.M., Sheffield V.C., Stone E.M.; "Characterization and comparison of the human and mouse GLCIA glaucoma
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANT ALA-164.
STRAIN=BALB/CJ, C3H/HeJ, and C57BL/6J; TISSUE=Brain, and Muscle;
MEDLINE=98249809; PubMed=9588210;
TOMATCA S.I., Tamm E.R., Chang B.;
"Characterization of the mouse Myoc/Tigr gene.";
Biochem. Biophys. Res. Commun. 245:887-893(1998).
                                                                                                                                                    070624; 070289;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Myocilin precursor (Trabecular meshwork-induced glucocorticoid response protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
MEDLINE=98345432; PubMed=9680392;
Abderrahim H., Jaramillo-Babb V.L., Zhou Z., Vollrath
"Characterization of the murine TIGR/myocilin gene.";
"mmm. Genome 9:673-675(1998).
                                                                                                                                      490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF041335; AAC32805.1; -.
EMBL; AF041333; AAC32805.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 8:377-384 (1998).
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129/Sv
                                                                                                                                                                                                                                                                                                                                MYOC OR TIGR
                                                                                                                                   MYOC MOUSE
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469 GGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAGCTGCCA 410
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145 LeugluGInGluAsnGluAspLeuAlaArgArgLeuGluSerSerGluGluValThr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATA---TCATCGGGGATGCTTTCTGG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GACAAGAAT 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 GAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGAAA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 ArgLeuArg-ArgGlyGlnCysProSerThrGlnTyrProSerGlnAspMetLeuProGl 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A---AGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCAGTTCTG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 GTGTGCTTAACCATGCAAGCCCTCCCACCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 CATCCCTACCACCCAGGACACTGGTGCGAATGACACAACTCAAGTTGGGAGGGGAACAGG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGGAAGGGATGGATGGGGGTGGTGTATCTTACTCTGTTTAAGCAGAACACCTTGTTTG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 uValProAlaSerGlnIleLeuLysGluAsnProSer-----GlyArgProArgSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluThrGlnThrArgAspLeuGluAlaAlaTyrAsnAsnLeuLeuArg------
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                                                                                                                                                                                                                  COILED COIL (POTENTIAL).
OLFACTOMEDIN-LIKE.
N-LINKED (GLCNAC. .) (POTENTIAL)
T -> A (IN STRAIN BALB/CJ).
2F090571E97B0425 CRC64;
                                                                                                                                                                                                                                                                                                                                      4490
1490
63
63
                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                 Coiled coil; Glycoprotein; Signal; Polymorphism.
SIGNAL 1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574 CAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1570 AA
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            224 riysgludiyAspLysdly----
                                                                                                MGD; MGI:1202864; Myoc.
InterPro; IPRO03112; Olfac_like.
Pfam; PF02191; OLF; 1.
SMART; SM00284; OLF; 1.
                                                                                                                                                                                                                                                     43 N-
164 T
55314 MW;
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76.00
33.87
26.34
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                                                                                                                                                                                                                                   490
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AF041334; AF049796;
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43
164
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P3K1 DICDI
ID P3K1 DICDI
AC P54673;
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SEQUENCE
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DB:
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ATGGCAGTGACCCGGACCAGGACCAGTGCCCTTGCACTGCGATATCATCGGGGAT 329

869

877

--SerSer

--ileLysAspileAspSer

GTTCTGGTGTGCTTA--

---ACCATG 248

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842 GlnIleThrHisIleSerIleArgGluIleLysLysProPheArgVal-----LysVal 859
                                508 AACATCAACTATAATAATGAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG 449
                                                                                                                                                                                                                                                                                                   |||::::||| :::
878 VallleValSerIleSerLeuTyrHisGlyIleGluCysPheSerLysAlaPheThrGln 897
                                                                                                                                                                                                                                                                                                                                             247 CAAGCCCTCCCACCTCCCAGGGCTCCTTGCCTTAGGTGGCTGTAGCATCCCTACCACCCA 188
                                                                                                                                                                                                                  328 GCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTGCGCTTCA
                                                                                                                                                                                     860 MetGlySerThrArg-------IleProLeuSerCys----
                                                                                                                                                                                                                                                                                                                                                              187 GGACACTGGTGCGAA 173
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                                                                                                                                                                                                                               Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
"A phosphatidylinositol (PI) Kinase gene family in Dictyostelium
discoideum: biological roles of putative mammalian pilo and yeast
Vp534 PI 3-kinase honologs during growth and development.";
Mol. Cell. Biol. 15:5645-5656(1995).
-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Phosphatidylinositol 3-kinase 1 (EC 2.7.1.137) (PI3-kinase)
PIKA OR PIKI:
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W; 55B678B72B34D783 CRC64;
                                                                                                                                                                                                                                                                                                                             1-phosphatidyl-1D-myo-inositol 3-phosphate.
-!- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
                                                                                                                   Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DictyDb, DD01099, pikA.
InterPro; IPR002420, PI3K_C2.
InterPro; IPR00341, PI3K ras_bind.
InterPro; IPR001263; PI3Ka.
InterPro; IPR001263; PI3Ka.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
Pfam; PF00454; PI3 PI4 kinase; 1.
Pfam; PF00613; PI3 PI4 kinase; 1.
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POLY-ASN
POLY-THR
POLY-THR
POLY-ASN
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                                                                                                                                                                                                                  MEDLINE=96009592; PubMed=7565716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00792; PI3K_C2; 1.
Pfam; PF00794; PI3K_rbd; 1.
SMART; SM00142; PI3K_rbd; 1.
SMART; SM00144; PI3K_rbd; 1.
SMART; SM00145; PI3Ka; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U23476; AAA85721.1; -.
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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1570 32 12 27 54

Length:
Matches:
Conservative:
Mismatches:
Indels:

10.2 76.00 35.20% 25.60%

Best Local Similarity:

Query Match:

Percent Similarity

Pred. No.:

US-09-914-191-1 (1-598) x P3K1_DICDI (1-1570)

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9, 2003, 12:48:48
913 ValAspirpCysGlu 917
                                                          Search completed: July
Job time : 22 secs
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Q99215 arabidopsis
Q9785 arabidopsis
Q9787 bomby mori
Q92171 mus musculu
Q92171 mus musculu
Q91677 homo sapien
Q2742 arabidopsis
Q957Q8 arabidopsis
Q957Q8 arabidopsis
Q957Q8 arabidopsis
Q957Q8 arabidopsis
Q952G bomby mori
Q89276 bomby mori
Q96114 pichia past
Q96114 pichia past
Q96114 pichia past
Q96109 homo sapien
Q96101 caenorhabdi
Q9775 bacillus ha
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Q9wmby artus norv
Q9upc2 homo sapien
Q96aw0 homo sapien
Q964w6 mus musculu
Q8478 chlamydia t
Q9pjs1 chlamydia m
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Q12393 saccharomyc
Q60021 thermus aqu
Q9fgw5 arabidopsis
Q85735 murine type
Q9c2a4 neurospora
                                                                                               O9v3n8 drosophila
O9y7t3 schizosacch
O9siq0 arabidopsis
O9zv61 arabidopsis
                                                Q9cqt0 mus musculu
Q9cy52 mus musculu
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Q94hv6 oryza sativ
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ13293 fis, clone OVARC1001188 (Similar to hypothetical protein FLJ20546) (Hypothetical 20.2 kDa protein)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo.
  29h0s2
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  Q9H8R6
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-MODEL=frame+ n2p-model -DEV=x1p
-MODEL=frame+ n2p-model -DEV=x1p
-MODEL=frame+ n2p-model -DEV=x1p
-Q=/Cgn2 1/USFO_spool/USO9914191/runat_09072003 112349_12876/app_query.fasta_1.775
-DB=SFREMBL_21 -QFMT=fastan -SURFIX=rspt -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -STRXT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -STRXT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -STRXT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-UNO WMAP -LARGEQUERY -NEG_SCORES=0 - MAIT -DSPELOCK=170 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=0 - THRENDS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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(c) 1993 - 2003 Compugen Ltd.
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                             CAACAATCTGGACTAACACCCAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCA
                                                                                                                                                                                                                                                                                538 GACAAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATG
                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=BRAIN;
MEDLINE=21154917; PubMed=11230166;
Midmann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
Wambutt R., Korn B., Klein M., Pouetka A.;
"Towards a Catalog of Human Genes and Proteins: Sequencing and
                                                                      Straubberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK023135; BAB14540.1;
EMBL; BCO01852; AAH01652.1;
EMBL; BC001523; AAH01523.1;
                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                        ll protein.
173 AA; 20157 MW; 70C1D8FFC116B416 CRC64;
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103
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 34.8 kDa protein.
DKF2P564B1172.
                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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Gaps:
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544.00
99.04%
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                                    Submitted (JAN-2001)
                                                      SEQUENCE FROM N.A.
TISSUE=MUSCLE;
                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
       SEQUENCE FROM N.A
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                  TISSUE=MUSCLE;
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SEQUENCE 17
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Pred. No.:
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Q9H0S2;
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235 TyrArgLysGlyThrValLeulleTrpGlnLysValAspGluValMetThrLysGlulle
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"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

"BEMBL; AR000553; BAB312870.1;

"BEMBL; AR021663; BAB13870.1;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human CDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).

EMBL; AL136669; CAB66604.1; -.

Hypothetical protein.

SEQUENCE 298 AA; 34831 MW; A6C941B75611C448 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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Matches:
Conservative:
Mismatches:
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Query Match:
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TISSUE=EMBRYO;
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EMBL; AK016076; BAB30104.1; -.
EMBL; AK015467; BAB2959.1; -.
EMBL; AK015467; BAB2959.1; -.
EMBL; AK015467; SA009607Rik.
SEQUENCE 238 AA; 27998 MW; S
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5730409G07RIK.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                538 GACAAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATG
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AA; 34815 MW; A6C951E716019408 CRC64;
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MEDLINE=21085660; PubMed=11217851;
                                                                2.34e-51
537.00
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5730409G07RIK.
Mus musculus (Mouse).
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                                          Alignment Scores:
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SEQUENCE FROWN N. S. STRAIN-CSTRL/GS; TRAIN-CSTRL/GS; TISSUE=EMBRYONIC LIVER; MEDLINE-21085660; PubMed=11217851; MEDLINE-257BL/GS; TISSUE=EMBRYONIC LIVER; MEDLINE-257BL/GS; TISSUE A., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aarawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kochiwa H., Kadota K., Matsuda H.A., Sasito T., Gissi C., King B., Kochiwa H., A., Staubi F., Suzuki R., Tomita M., Magner L., Washio T., Asakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Bakai K., Okido T., Putuno M., Aono H., Baldarelli R., Barsh G., A Buke J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Willming L., Aynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                           3.95e-39
                                                                                                                    428.00
89.42%
76.92%
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Query Match:
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Adams M.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Ann K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Ann K.H., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
61-MAR-2001 (TrEMBLrel. 16, Last annotation update)
62-D500929-4 protein.
62-D500929-4 OR C4103-
63-D500929-4 OR C4103-
64-D500929-4 OR 
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK010876; BAB27240.1; -.
MGD; MGI:1913878; 5730409G07Rik.
SEQUENCE 298 AA; 34971 MW; D4CAOC154E452ECA CRC64;
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113
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Mismatches:
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Matches:
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                                                                                                                                                                    4.06e-39
428.00
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                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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535 AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT 476
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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Calodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris M., Harris M.D., Harvey D., Heiman T.J., Mei M.-H., Ibegwam C., Alalin M., Kalubak F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Karfet C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reses M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Shen H., Alvelson K., Saunders R.D.C., Scheeler F., Shen H., Shie B.C., Siden Kiamogon K., Saunders R.D.C., Scheeler F., Shan H., Shie B.C., Siden Kiamogon I., Simpson M., Strong R., Sun E., Spier B., Spradling A.C., Staplecon M., Strong R., Wang X., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng W., Zhong K.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zha S., Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99403001; PubMed=10471707; Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvay D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw F., Rubin G.M.;

"An exploration of the sequence of a 2.9-Mb region of the genome of Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         il protein.
286 Aa; 33072 MW; 9539693DA9C2BFC8 CRC64;
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13
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18
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Matches:
Conservative:
Mismatches:
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FlyBase; FBgn0028925; BG:DS00929.4.
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219.00
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Best Local Similarity:
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SEQUENCE 28
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Q9Y7T3

RESULT Q9Y7T3

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LysSerGlyLysSerValSerGluThrGlnGlulleLeuLysAspThrGlnLysGlnGln 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATCTGGACTAACACCCGAGTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGGCTGCCGATGTAT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTTGCACTGCGAT---ATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Srreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
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LysAsnGluLeuLeuPheGlnLysPheGlyIleAsnTyrLysThrLeuProGluLeuPhe
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Lin X., Kaul B., Shaa T.P., Fujii C.Y., Shen M., VanAken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC007011, AAD24854.2;
                                                                                                                                                                                                                                                                                                         E75CABDB892453BE CRC64;
                                                                                                                                                                                                                                                                                                                                                   495
32
21
40
9
                  01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 57.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
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Mismatches:
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Matches:
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      Created)
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                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 495 AA; 57942 MW;
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129.50
51.96%
31.37%
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      (TrEMBLrel. 13,
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258 AsnAsp 259
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Best Local Similarity:
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAATGAGATTTTGTTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 AGGAAAGGGACTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCCAACAGAAATGGAAGGAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTG
                                                                           ----SerArgGlnAlaValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATCTGGACTAACACCCAGTACAAGCCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                             Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy L., Harris D., Wood V., Rajandream M.A., Barrell Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. - I- SIMILARITY: TO YEAST YGRO24¢. EMBL, AL049522; CAB40011.1; -. Hypothetical protein.
                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypotherical 31.1 kDa protein C63.07 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 protein.
261 AA; 31063 MW; FCC4B047C3D2D7DA CRC64;
                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae, Schizosaccharomyces.
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222
32
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Conservative:
Mismatches:
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Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                               PRT;
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169.50
59.41%
37.62%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTA 299
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=972;
                                             415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Query Match: DB:

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Percent Similarity:
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Saguence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                              :::||||||| ::: :::|||||||| ::: 227 LysSerGlyLysSerLysInglnThrArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                              CAATCTGGACTAACACCCAGGTACAAGCCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGAC
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAATGAGATTTTGTTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECKET J.R.;
"Arabidopsis cDNA clones.";
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AYOS6804; AAL10495.1;
InterPro; IPR003851; Znf_Dof.
                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                            EMBL; ACO05700; AAC69945.1; -.
SEQUENCE 297 AA; 34814 MW; E7581E66D57A7DA3 CRC64;
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                                                                                                                                                                                                                                                                                    297
20
112
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                  0.129
94.00
62.75%
39.22%
8.51%
                                                                                                                                           Nature 402:761-768(1999).
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SEQUENCE 457 AA; 499
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
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Length:

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190
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                                                                                                                                                                                                    |||||||
267 ValProLeuAsnGlnThrAsnGluGluAlaArgThrVal----SerProLeuProLys 284
                                                                                                                                                                                                                                                                                                        304
                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 GTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCACCCCCATCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190
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305 ThrIleLeuProPheTyrProProPlaTyrTrpSerCysProGlyValSerProGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 ATCCCTTCCCTGCTCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGG
                                                                                                                                                                                                                                                               131 ATCCCTTCCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACAGTGTCCTGG
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones.";
DNA Res. 5:203-216(1998).
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28
5
32
27
  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similarity to H-protein promoter binding factor.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 ITCAICTAGAAICTCTGGAIGTICCTICCAGAAAGC 328
                                                                                                                                                                                                                                                                                                                                                  191 GTGGTAGGGATGCTACAGCCACCTAAGGCAAGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                    Conservative:
Mismatches:
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Matches:
  Matches:
                                                                  Indels:
                                                                                                                               x Q93ZL5 (1-457)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 AlarrpAsnSerPhe-----
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InterPro; IPR003881; Znf. Dof.
Pfam; PF02701; zf-Dof; 1.
SEQUENCE 515 AA; 56528 MW;
88.50
35.87%
30.43%
8.07%
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88.50
35.87
30.43
8.07
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|GInArgLeuLeuAlaSerAlaLeuGlnIleHisArgPheHisProCysTrpProLysGly 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AGCCACCTAAGGCAAGGAGCCCCTGGGAGGTGGGAGGCCTTGCATGGTTAAGCACACCAGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 ACTGAAGCGCAAAAGGGTCAGCTGTTTCATCT-----AGAATCTCTGGATGTTCCTTC 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATAG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | |
| MetGlyGlnArgProGlnThrPheAsnSerSerAlaThrValSerLeuSerGlyThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 TyrserThrdinValLeuLeuArgGluValTyrGinSerPro------CysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 AsnAlaAlaLeuCysArgAspLeuValSerGlyLeuPheAsnIleSerSerCysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGCTGNAAGAGTTCCCTGTAAT
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SerGinCysSerPheAsnGly-----
                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                      495 AA; 54319 MW; A76468A0CBF86AAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Ectonucleoside triphosphate diphosphohydrolase 2.
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                 PROSITE; PS01238; GDA1_CD39_NTPASE; UNKNOWN_1
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                                                                                                                                                                                                                                          MGD; MGI:1096863; Entpd2.
InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
 Created)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2001) to the
EMBL; BC011241; AAH11241.1;
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84.50
37.80%
25.61%
7.71%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                      Mus musculus (Mouse)
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                       Hydrolase.
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Q9LP79;
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                                                                                    233 AGGIGGGAGGGCTTGCATGGTTAAGCACCACAGAACTGAAGGGCAAAAGGGTCAGCTGTC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::::::::::||| :::
136 IleGluSerGluGlyGluMetAsnAspThrProGlnAspAspGluAlaGluLysLysAsp 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 ThrileLeuProPheTyrProProProAlaTyrTrpSerCysProGlyValSerProGly 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 TCTGAATTCAACATCAACTATAATAAT-----GAGCTGCCGATGTATAGGAAAGGG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 ACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAGCTGCCAACA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 GAAATGGAAGGAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTGCCCTTGCAC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 TGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGC 287
                    --- AGCCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACAAGCCCAAGGGAGATTACAGGGAACTCTTNCAGCAGACAAGAATGAGATTTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hagiwara K., Tomita M., Kobayashi J., Miyajima S., Yoshimura T.;
"Nucleotide sequences of Bombyx mori cytoplasmic polyhedrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B172F1D7E790E2B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330
727
724
843
88
                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   Bombyx mori cytoplasmic polyhedrosis virus (BmCPV).
Viruses; dsRNA viruses; Reoviridae; Cypovirus.
VCBI_TaxID=31594;
                                                                                                                                                         TTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGC 328
                                                                                                                                                                                          ------ThrTrpMetProGlnProAsnSer 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             segment 8.";
Biochem. Biophys. Res. Commun. 247:549-553(1998)
EMBL; AB016437; BAA32043.1; -.
SEQUENCE 390 AA; 44151 MW; B172F1D7E790E2B9
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Matches:
Conservative:
Mismatches:
Indels:
                  191 GTGGTAGGGATGCTACAGCCACCTAAGGCAAGG-
                                                                                                                                                                                                                                                                  390 AA
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                                                                                                                       325 AlarrpAsnSerPhe------
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01-NOV-1998 (TrEMBLrel
01-DEC-2001 (TrEMBLrel
Non-structual protein
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Q921R1;
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 GGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 TTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGAT 312
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| LeuSerLeuProProSerProProAlaSerSerThrPheAlaThrArgHisLysLeuAsp 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC020893, AAF79694.1;
                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 CCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCTGGGT
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
Chao O., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Pederspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic sequence for Arabidopsis thaliana BAC TIN15 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
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343 AA; 38371 MW; CE0EAC1EA62DB64B CRC64;
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62
65
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Conservative:
Mismatches:
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                                                   Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-914-191-1 (1-598) x Q9LP79 (1-343)
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Submitted (JAN-2000)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=3702;
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1204 LeuAlaArgLysHisSerLeuThrLysAsnAsp---SerSerProGln---ArgCysSer 1221
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                                                                                               129 LeulleSerSerLeulleLeuProGlnPhePheLeuSerGlylleIleGluAlaThrPhe 148
                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINEE20450683; PubMed=10997877;

MEDLINEE20450683; PubMed=10997877;

Magase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human genes.

"XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 7:273-281(2000).
109 ValSerAlaProPheGlnGluLysGlySerPheLeuTrpValLeuAlaProValVal
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                                                      CTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1628 AA; 174427 MW; 4E23A34360A3D939 CRC64;
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43
24
77
72
9
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Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                               472 TCCTATACATCGCCAGCTCATTATTAGT 501
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HSSP; P15822; IBBO.
InterPro; IPR000822; Znf_C2H2.
Pfam; PP00096; zf_C2H2; Z.
SMART; SM00355; ZnF_CZH2; z.
PROSITE; PS00028; ZINC_FINGER_C2H2_1: 1.
PROSITE; PS0157; ZINC_FINGER_C2H2_2; 2.
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1262 CysProLeuGlyArgGluLeuAlaProArgAlaHisValLeuSerLysLeuGluGlyThr 1281	188TGGGTGGTAGGATGCTACAG 208		09CCACCTAAGGCAAGGAGCCTGGGAGGGGGGGGGGCTTGCATGGTTAAGCACACAG 20	::::: 1302 SerProProArgSerAlaProProGlyLysTrpAlaLeuAlaGlyProGlySerPro 1320	266 AACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGATGTTCCTTCC	:::	326 AGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGT367		88		33TGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGT 4		1 CATCACTICATCCACCTICTGCCATATCAACACACACTCCTTTCCTATA 478	
126	18	128	20	130	26	132	32	134	36	136	38	138	43	140
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Search completed: July 9, 2003, 12:50:28 Job time : 53.5 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 12, 2003, 13:00:53 ; Search time 1245 Seconds (without alignments) 13978.697 Million cell updates/sec Run on:

US-09-914-191-1 598 Title: Perfect score:

1 ttggaatagttcttgcttta......ggtgttagtccagattgttg 598 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Sequence:

Scoring table:

2054640 seqs, 14551402878 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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ALIGNMENTS

PAT 22-SEP-2000 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. linear DNA AX034339 598 bp Sequence 1 from Patent W00050637. AX034339 AX034339.1 GI:10303095 human. RESULT 1
AX034339
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
VERSION
CEYWORDS
SOUNCE
ORGANISM

1 (bases 1 to 598) Godson,C.M., Brady,H.R. and Martin,F.M. Identification of genes having a role in the presentation of diabetic nephropathy

REFERENCE AUTHORS TITLE

```
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                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 3 Row: b Column: 4.
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Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadamageystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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/tlb home="mino" pa
                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1208)
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Submitted (21-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGNAAGAGTICCCTGTAAICTCCCTTGGGCTTGTACTGGTGTTAGTCCAGAITGTTG 598
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Patent: WO 0050637-A 1 31-AUG-2000;
GODSON CATHERINE MARY (IE) ; BRADY HUCH REDMOND (IE) ; HIBERGEN
LIMITED (IE) ; MARTIN FINIAN MARY (IE) ; UNIV COLLEGE DUBLIN
NATIONAL U (IE)
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	Oy 481 TGGGCAGCTCATTATTATAGTTGATGTTGAAAATCAAAATCTCATTCTTGTCTG 540	N Homo sapiens CDNA FLJ20546 IIS, AK000553. GI:7020725 Oligo capping; fis (full insert Homo sapiens signet-ring cell ca mRNA, clone lib:KAT clone:KAT115 M Homo sapiens Eukaryota; Metazoa; Chordata; CI Mammalia; Eutheria; Primates; C3 1 (sites) Watanabe,K., Kumagai,A., Itakura Ota,T., Suzuki,Y., Obayashi,M., Nakamura,Y., Isogai,T. and Sugai NEDO human cDNA sequencing proje	DOURNAL Unpublished REPERENCE 2 (bases I to 1233) AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y. Shibahara, T., Tanaka, T. and Nakamura, Y. TITLE Direct Submission JOURNAL University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minatc-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416) NEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency). Location/Qualifiers Location/Qu
QY 481 TCGGCAGCTCATTATTATGTTGAATTCAGAAACCAAAATCTCTTGTCTG 540	USA REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov COMMENT Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The Li M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadamsbiology.org Anup Madan, Rachel Diockhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Ketteman and Anuradha Madan	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 10 Row: g Column: 20. Location/Qualifiers 1. 1208 /organism="Homo sapiens" / db xref="Homo sapiens" / clone="MGC:4529 IMAGE:3010614" / tissue type="Muscle, rhabdomyosarcoma" / clone="MGC:4529 IMAGE:47" / lab host="DH10B-R" / lab host="DH10B-R" / location: pOTB7"	/codon start=1 /product="similar to hypothetical protein FLJ20546" /protein_id="AAH01852.1" /db_xref="dd" AAH01852.1" /db_xref="dd" AAH01852.1" /translation="WHTWHORGAPSYPFWRDYPEDQPLLYPPGFDGRVVVPPSNQTL KOYLSWRQADCHINNLYMYVPMALIOQSGLTPVQAGRUGGTLAADKNBILFSFENIN YNNELPHYRGGTVLIWGKVDEVWTKEIKLPTEMEGKKMAVTRTRTKPVPLHCDIIGDA FWKEHPPELLDEDS" PWKEHPPELLDEDS" Query Match 99.8%; Score 597; DB 9; Length 1208; Best Local Similarity 99.8%; Pred. No. 2.7e-160; Matches 597; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 597; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 TTGGAATAGTTCTTGCTTTATAAAAATAGTACTGCGATTAAAAAAAA

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Direct Submission
Submitted (16-FB3-2000) Takao Isogai, Helix Research Institute,
Submitted (16-FB3-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 153-23 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NBDO human cDNA sequencing project supported by Ministry of
Enternational Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology; CDNA library
construction, 5'-& 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
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                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                   Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., and Oshima, A. NDO, human cDNA sequencing project
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Pred. No. 1.3e-158;
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/note="cloning vector: pME18SFL3"
463 c 522 g 567 t
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/db_xref="taxon:9606"
/clone="HEMBA1002267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
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LHCDIIGDAFWKEHPEILDEDS"
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to Sus scrofa decorin mRNA.
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oligo capping; fis (full insert sequence).
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                                                                                                                                                                                                                                                                                                                           121 ACCCCATCCATCCCTTCCCTGTTCCCCTCCCACTTGAGTTGTGTCATTCGCACC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 598
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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
                                                                                                                                                                                                                                                                                                                                                                         1080 ACCCCATCCATCCCTTCCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACC
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Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA
mRNA, clone_lib:HEMBA1 clone:HEMBA1003893.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAAGTCCAGATTGTTG
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                                         Length 1216;
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Homo sapiens cDNA FLJ11601 fis, clone HEMBAl003893.
AK021663
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                                         DB 9;
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                                         Score 590.6; DB 9;
Pred. No. 1.9e-158;
0; Mismatches 5;
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gai, T. and Otsuki, T.
                                       98.8%;
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (PKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Project.
This clone (DKEZDSE4B1172) is available at the RZPD in Berlin.
Please contact the RZPD. Ressourcenzentrum, Heubnerweg 6, 14059
Please contact the RZPD. Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/CDNA/.
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/product="hypochetical_protein"
/product="hypochetical_tologold"
/protein_id="Cab66604.1"
/db_xxef="c01:12052862"
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PTCLAHGWAVVRLDGRNFHRPAEKHNPAKPNSAPAQLMTKAQTVWBELBIDIVIAYG
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VYYPSNGTLKGYLASWGADGHLNNLYNTVFWALIQQSGLTPVQAQGTLAADKNB
ILFSENINYNNELPMYRKGTVLIWQKVDEVMTKEIKLPTEMBGKKWAVTRTRTKPVP
                             CGGCGGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC 1248
                                                                                                                                                                                                                                                        1216 bp mRNA linear PRI 10-MAR-2001 mRNA; cDNA DKFZp564B1172 (from clone DKFZp564B1172);
CGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC 541
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1 (bases 1 to 1216)
Wiemann,S., Weil,B., Wellenreuther,R., Gassenhuber,J., Glassl,S., Ansorge,W., Boecher,M.; Bloecker,H., Bauersachs,S., Blum,H., Lauber,J.; Duesterhoeft,A., Beyer,A., Koehrer,K., Strack,N., Mewes,H.W., Ottenwaelder,B., Obermaier,B., Tampe,J., Heubner,D., Vonard a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S
                                                                                                                      1247 TGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 1191
                                                                                           598
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/tissue_type="brain"
/clone_lib==1564 (synonym: hfbr2). Vector pAMP1; host
X1-2blue; sites NotI + SalI"
                                                                                        TGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG
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Submitted (15-DEC-2000) MIPS, Am Klopferspitz 18a, D-82152
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/db_xref="taxon:9606"
/map="5"
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Isogai, T. and Otsuki, T.

Burect Submitssion
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@bri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; ONA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5' & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                        01-AUG-2002
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KDYLSWRQADCHINNLYNTVFWALIQOSGLTPVQAQGRLQGTLAADKNEILFSEFNIN
YNNELPWYRKGTVLIWQKVDEVWTKEIKLPTEMEGKKMAVTRTRTKPVPLHCDIIGDA
                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawaza, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Waxamatsu, A., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project
  Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           oligo capping; fis (full insert sequence)
Homo sapiens ovary, tumor tissue cDNA to mRNA, clone_lib:OVARC1
clone:OVARC1001188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         744 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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                                                                                                                                                      AK023355 1780 bp mRNA linear
Homo sapiens cDNA FLJ13293 fis, clone OVARC1001188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="ovary, tumor tissue"
/clone Tib="OVARC1"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 504; DB 9; L
Pred. No. 1.4e-133;
O; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/protein_id="BAB14540.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="OVARC1001188"
                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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nilarity 93.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 555; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513
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VERSION
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ORIGIN
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AK023355/c
                                                                                                                                                                                                                                                                                                                                   ORGANISM
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REFERENCE
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                           KEYWORDS
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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Mnistry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /procein_id="Bab13870.1"
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VVYPSNQTLKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTLAADKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,005
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LHCDIIGDAFWKEHPEILDEDS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   764 ATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATAC 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 CCCCCATCCATCCTTCCTTCCTTTCCCTCCCAAC - TTGAGTTGTGTCATTCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCCAAGGAGCCCTGGGAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 AGGCCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              944 AGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 884 AGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.6%; Score 577.6; DB 9; Length 2263; 98.8%; Pred. No. 1e-154; ive 0; Mismatches 5; Indels 2;
                                                                                                                                                                                                                                                                                                                                                        /tissue type="whole embryo, mainly head"/clone_lib="HEMBA1"
                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="embryo, 10 weeks"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4. .900
/note="unnamed protein product"
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                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1003893"
                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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Best Local (
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Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
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                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                              Full Clone Sequencing of the Longest Available Member from Each
Unigene Cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                             108074 CCCCCATCCATCCTTCCTTCCTGTTCCCCTCCCCAACTTGAGTTGTGTCATTCGCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTCCTGGGTAGGGATAGCTACAGCCACCTAAGGCAAGGAGCCCTGGGGAGGTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108254 AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108194 GGCTTGCATGGTTAAGCACCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCCATCCATCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTITIGLCCTGGTCCGGGTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT
                                                                                                                                                                                                                                                                                                                                                     AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                ö
                                                                                                                                                                                      Length 155344;
                                                                                                                                                                                                                                                                         אנאים אנאם אוא אואס אואס linear
Homo sapiens full length insert cDNA clone ZD93F03.
AF086486
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 447; DB 9; I
Pred. No. 4.1e-117;
0; Mismatches 5;
                                                                                                                             u
                                                                                                     /clone="CTC-370J7"
45174.a 30884 c 31469 g 47817
                         1. .155344
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
      Location/Qualifiers
                                                                                                                                                                                    74.7%;
illarity 98.9%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF086486.1 GI:3483831
FLI CDNA.
Homo sapiens.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa,
Mammalia, Eutheria,
1 (bases 1 to 416)
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Waterston, R.
                                                                                                                                                                                                         Similarity
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Homo sapiens chromosome 5 clone CTC-370J7, complete sequence.
AC026407
MC026407.4 GI:15375158
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

3 (bases 1 to 155344)

DOE Joint Genome Institute and Stanford Human Genome Center.
CCCCCATCCATCCTTCCTTCCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACCA 625
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Submitted (18-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Brive, Walnut Creek, CA 94598, USA
4 (bases 1 to 15534)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (30-A002-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:14861724.
Draft Sequence Produced by DOE Joint Genome Institute
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                              242 GGCTTGCATGGTTAAGCACACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG
                                          GIGICCIGGGIAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAG
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DOE Joint Genome Institute and Stanford Human Genome Center
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
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WI-6759 G05738
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241 GGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA 300
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Pred. No. 2.3e-95;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                       Initial incubation: 95 degrees C for 10 minutes
                                                                                                                                                                                                                                                                                                                                                                                seconds
                                                                                                                              Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259687
Fax: 4157259689
Fax: 4157259689
Finer A: CAACACCGCAAACAGGTGT
Primer B: GCTTAACCATGCAAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       each 1 uM
each 200 uM
0.07 units/ul
5 ul
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23
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60 degrees C for 30
72 degrees C for 23
30
Perkin Elmer 9700
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                                                                                                              Stanford Human Genome Center (SHGC)
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Total Vol:
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/map="5"
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75. .258
                                                                                               Contact: Richard M. Myers
                                                                                                                                                                                                                                                                                                                                           Denaturation:
Annealing:
Polymerization:
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Thermal Cycler:
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Best Local Similarity 99.5%;
Matches 372; Conservative
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                                                      Unpublished (1998)
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                   Myers, R.M.
Human STSs (1998)
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SHGC-58349 Human Homo sapiens STS genomic, sequence tagged site.
G38490
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                                                                                                                            NOTICE: This sequence represents the full insert of this CDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved.

Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGAATAGTTCTTGCTTTATAAAAATAGTACTGCGATTAAAAAAAGGCACTTCTGCCA 349
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IWAGE:357053"
/clone lib="Soares fetal heart_NDHH19W"
/ 0100 01 0109 0103 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%; Score 406.4; DB 9;
99.8%; Pred. No. 1.4e-105;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                            The location of this clone is unknown Location/Qualifiers
                                                      St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
Genome Sequencing Center
Department of Genetics
Washington University
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Gaps

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Qy 2 TGGAATAGTTCTTGCTTTATAAAAATAGTACTGCGATTAAAAAAAA	122 CCCCCATCCATCCATCCTTCCTTCCCTCCCCAACTTGAGTTGTGTCATTCGCACCA 181	257 CTTTGTCCTGGTCCGGGTCACTGCCATATCCATCTTTTTTCTTTGTTGTTGCACTTACT 422 TTCTTTTGTCCTGGTCCGGGTCACTGCCATATCACACACA	E OR I
Qy 301 GAATCTCTGGATGTTCCTTCCAGAAAGCATCCCGATGATATCGCAGTGCAAGGGCACTG 360 Db 301 GAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCATGG 360 Qy 361 GCTTTGTCCTGGTC 374 Db 361 GCTTTGTCCTGGTC 374	RESULT 12 G3734 LOCUS LOCUS LOCUS DEFINITION SHGC-57583 Human Homo sapiens STS genomic, sequence tagged site. ACCESSION G37344 G3734 G373	Contact: Richard M. Myers Stanford Human Genome Center (SHGC) Stanford University School of Medicine Department of Genetics, M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689 Email: myers@shgc.stanford.edu Primer A: CAACACGCAAACAAGGTGT Primer B: TCCTTGCCTTAGGTGGTGT STS size: 150 PCR Profile: Initial incubation: 95 degrees C for 10 minutes Denaturation: 94 degrees C for 30 seconds Annealing: 60 degrees C for 30 seconds PCR Cycles: 72 degrees C for 23 seconds PCR Cycles: 97 Perkin Elmer 9700 Protocol: Primer: Perkin Elmer 9700 Protocol: 25 ng Thermal Cycler: Perkin Elmer 9700 Protocol: 25 ng Thamplate: 25 ng Primer: Hamplate: 25 ng Ampliraq Gold Polymerase: 0.07 units/ul Total Vol: 5 ul	2.5 mM 50 mM 4Cl: 10 mM 8.3 primer pairs derived 10n/Qualifiers 567 anism="Homo sapiens" xref="taxon:9606" "5" 128 188 198 198 194 c 119 g 161 144 c 119 g 161

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musers I (bases I to 318930)

RS Metzker, M.L. Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomaes, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pacce, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Bubay, C., Burkett, C., Chon, G., Chen, G., Chen, G., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Ferrandacz, C., Perraguto, D., Forcum-Tanesy, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M., Hobask, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Massey, E., McLeod, M. P., Mei, G., Moore, S., Morgan, M., Martin, R., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B., Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Nres, M., Scherer, S., Sodergren, E., Weinstock, G., Nree, S., Walter, S., Shen, H., Wengeren, E., Weinstock, G., Niver, S., Shen, R., Anderson, A., Mree, S., Martin, C., Shen, R., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-primer Bodipy: 71% of reads
Chemistry: Dye-primer Bodipy: 71% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 292670 bases at least Q40
Consensus quality: 299603 bases at least Q30
Consensus quality: 299603 bases at least Q30
Consensus quality: 30271 bases at least Q30
Estimated insert size: 298164; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 5.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 15, 2000 this sequence version replaced gi:10800205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: RP23-345K4
AC073495.12 GI:10801940
HTG; HTGS PHASE1; HTGS_DRAFT
Mus musculus.
Mus musculus
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JOURNAL
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                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-298M7 is from the RPCI-23 Mouse PAC Library—constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6

This sequence is the entire insert of clone RP23-298M7 The true left end of clone RP23-298H5 is at 164150 in this sequence. The true right end of clone RP23-30215 is at 69639 in this sequence.
abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORWPEP; Information on the WORWPEP database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Sequence from uni-directional primer reads and dGTP
big dye terminator reads only."
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/note="Sequence from overlapping clone RP23-29H5
(AL663031). Assembly confirmed by restriction digest."
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/note="Sequence from overlapping clone RP23-29H5
(AL663031). Assembly confirmed by restriction digest."
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/note="Sequence from uni-directional dGTP big dye
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/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-298M7"
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                     Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                          Center clone name: CH230-92F20
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Human cDNA clone (Human prostate exp Human prostate exp

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Drosophila melanog Drosophila melanog Drosophila melanog

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Identifying genes used for identifying drugs for the prevention and/or therapy of diabetic nephropathy involves culturing mesangial cells in
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                        glucose 1) cDNA partial sequence. IHG-1 was identified using a novel method for identifying genes that have a role in the presentation of diabetic nephropathy (DN). This method involves culturing measangial cells in a medium in the presence of a concentration of glucose sufficient to induce differential expression of a gene susceptible to such differential expression, and identifying the gene so induced, especially by suppression subtractive hybridisation. Further portions of IHG-1 cDNA are given in AAA50409 and AAA50410. Genes identified by this method, including IHG-1, can be used as a diagnostic marker for the progression and presentation of DN, as an index of disease activity and the rate of progression of DN, and as a basis for identifying drugs for use in the prevention and/or therapy of DN (claimed).
                                                                       that of a human IHG-1 (increased in high
presence of glucose which induces differential expression of
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                                                     Claim 8; Page 7-8; 86pp; English.
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Matches 598; Conservative
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in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed
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                                                             gene therapy; cancer;
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Zhang J
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 597; DB 22;
Pred. No. 6.3e-174;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen R,
                            polynucleotide SEQ ID NO 170.
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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25-APR-2000; 2000US-0552117.
09-JUL-2000; 2000US-059042.
19-JUL-2000; 2000US-0623150.
                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                             26-DEC-2000; 2000WO-US34263
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Best Local Similarity 99.83
Matches 597; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and such as central nervous
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                                                                                                     Homo sapiens
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1162

AAIS7967/c ID AAIS7967 standard, cDNA, 1231 ! XX AC AAIS7967, Xy,

RESULT

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient, cancer in a patient,

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate call carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1246 GGCTTGCATGGTTAAGCACACCAGAACTGAAGGGCAAAAAGGGTCAGCTGTCTTCATCTAG 1187
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                                                                                                                                                                                                                  patient;(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                                                                                                                                                   Sequence 1512 BP; 407 A; 327 C; 401 G; 356 T; 21 other;
                                                                                                                                                                                                                                                                                                               Pred. No. 4.4e-173;
0; Mismatches 2;
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Best Local Similarity 99.7%;
Matches 595; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               624
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                       ACCCCCATCCATCCTTCCTTCCTGTTCCCTCCCAACTTGAGTTGTGTCTTCGCACC
   ACCCCCATCCATCCTTCCTTCCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACC
                                                                     AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGA
                                                                                        GGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA
                                                                                                                                                                 GGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA
                                                                                                                                                                                                   GAATCICTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
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ID ABV22854 standard; cDNA; 1512
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; 200US-189862P.
; 200US-207454P.
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pharmacogenomic marker;
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1186 AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG 1127
                                                                                                                                                                                                                      1066 TTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                          598
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                                                                                                                                                                                                                                                                                                              1006 CGGCGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                     482 CGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC
                                                                                                                                                                          TTCTTTTGTCATCACTTCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                  542 IGNAAGAGTICCCIGIAAICICCCTIGGGCTIGIACIGGIGITAGICCAGAITGIIG
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T.
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AAH13744 standard; cDNA; 2159
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999;
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                                                                                       362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH13744,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or invalue.
cytostatic; carcinogen; pharmacodyanamic marker;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccccarccarccrrccrrccrcrccrccrccrccaacrrcagragragrarcarrcgcacca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.4%; Score 594.4; DB 23; Length 1512; Local Similarity 99.7%; Pred. No. 4.4e-173; Length 1512; Les 595; Conservative 0; Migmatched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1512 BP; 407 A; 327 C; 401 G; 356 T; 21 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 6017; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE;
                                                                                                                                                                                                                                                                2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                 2000US-255281P.
                                                                                                                                                                                                                      20-FEB-2001; 2001WO-US05171
                       Human; prostate cancer;
pharmacogenomic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-662795/76
                                                                                                                                 WO200160860-A2
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                                                                                                                                                                                                                                                                  17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                            25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                          18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schlegel R,
                                                                                                                                                                             23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1367 TTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACACAGTCCCTTTCCTATACAT 1308
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in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH13424 to AAH13632 encomparement human cDNA sequences, AAB92446 to AAH95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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                                                                                                                                                                                                                                           Score 591.2; DB 22; Length 2159;
Pred. No. 5.1e-172;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                      Sequence 2159 BP; 607 A; 463 C; 522 G; 567 T; 0 other;
                                                                                                                                                                                                                                         Query Match

Best Local Similarity 99.3%;
Matches 593; Conservative
                                                                                                                                                                 the present invention.
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AGGAACCATGTTCCAACACGCAAACGAGTGTTCTGCTTAAACAAGGTAAGATACACCA
                                                                                                                                                                                                                                         CCCCCATCCATCCTTCCTTCCTGTTCCCCTCCCAACTTTTTGTTGTGTCATTCACAC
                                                                                                                                            AGGAACCATGTTCCAACACGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
                                                                                                                                                                                                                 CCCCCATCCATCCCTTCCTTCCCTGTTCCCCTCCCAAC--TTGAGTTGTGTCATTCGCAC
                                                                                                                                                                                                                                                                                      CAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGG
                                                                                                                                                                                                                                                                                                                CAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGCCAAGGAGCCCTGGGAGGTGG
                                                                      Best_Local Similarity 98.8%;
Matches 592; Conservative
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                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                     1247 TGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 1191
                                                                                                                                                                                                                                                                                  sequence SEQ ID NO:13474.
                                                                                                                                                                           BP
                                                                                                                                                                         AAH15315 standard; cDNA; 2263
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                  Human cDNA
                                                                                                                                                                                                           AAH15315;
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RESULT 6 AAH15315/c

239 945 299 885

Gaps

96.6%; Score 577.6; DB 22; Length 2263; 98.8%; Pred. No. 8.4e-168; ive 0; Mismatches 5; Indels 2;

Sequence 2263 BP; 624 A; 486 C; 580 G; 573 T; 0 other;

AGGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT 944 AGGGCTTGCATGCTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT

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EP1074617-A2 Homo sapiens

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptises: (a) an oligo-dT primer and an oligonuclectide complementary to the complementary strand of a polynuclectide comprises one of the 5602 nuclectide sequences defined in the specification, where the oligonuclectide comprises at least 15 nuclectides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 3'-end sequence complementary to the complementary strand of a polynuclectide which comprises a 3'-end sequence complementary to a polynuclectide which comprises a 3'-end sequence complementary to a polynuclectide comprises at least 15 nuclectides and the comprise oligonuclectide comprises at least 15 nuclectides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the proteins encoded by the full-length without any specialised methods. AAH136528 and converse the specialised methods. AAH136546 to AAH136286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                                                                                                                                                              Yamamoto
                                                                                                                                                                                                                                                                              Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID 13474; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                              Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                         Wakamatsu
                                                                                                                                                                                                                                                                            Isogai T, Nishikawa
Sugiyama T, Wakama
                                                                                        29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                   09-JUN-2000; 2000JP-0241899
                                             2000EP-0116126
                                                                                                                                                                                                                                 (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
                                             28-JUL-2000;
  07-FEB-2001,
                                                                                                                                                                                                                                                                            Ota T, Is
Ishii S,
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for

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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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99JP-0300253
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                                                                                                 Best Local Similarity 99.8
Matches 541; Conservative
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27-AUG-1999;
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                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P cypression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing contactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.
                              825
                                                         419
                                                                                                                                                                   539
                                                                                                                                                                                 704 ATCGGCGGCTCATTATATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCT 645
    AGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACT 359
                                                                                 ATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATAC 479
                                                                                                                                  764 ATTICITITGICATCATCATCCACCTICTGCCATATCAACACAGTCCCTTTCCTATAC 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                   GGCTTTGTCCTGGTCCGGGTCACTCTTTTTCCTTCCATTCTGTTGGCAGCTTA
                                                                                                                                                                 ATCGGCAGCTCATTATATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCT
                                                                                                                                                                                                                                   644 GCTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG
                                                                                                                                                                                                                    540 GCTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer antigen encoding cDNA SEQ ID NO:958.
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                                                                                                                                                                                                                                                                                                                 ВР.
                                                                                                                                                                                                                                                                                RESULT 7
AAH33902/c
ID AAH33902 standard; cDNA; 557 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0157137.
99US-0163280.
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                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       colorectal carcinoma; ss.
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P-PSDB; AAG74471.
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC 541
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                                                                                                                                                                      302 GGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAG
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                                                                                             Gaps
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                                             DB 22; Length 557;
                                                                                             0; Indels
Sequence 557 BP; 156 A; 111 C; 150 G; 139 T; 1 other;
                                             90.6%; Score 541.6; DB 22 99.8%; Pred. No. 5.6e-157;
                                                                                             1; Mismatches
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425 TTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT 366

422

482

542 TGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTAGTCCAGATTGTTG 598 TGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCCAGATGTTG 249

365 CGCCACCTATATATATAGTTGATGTTGAATTCAGAAACAAAATCTCATTCTTGTCTGC CGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGTCTGC

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RESULT 9
AAK90825/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprising as tleast 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                     the 5602
detection
                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs.
                                                                                                                                                                                                       Yamamoto J;
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Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 15323; 2537pp + CD ROM; English.
                                                                                                                                                                                                    Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                       Wakamatsu
                                                                                                                                                                                                    Nishikawa
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                     (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                    Ishii S, Sugiyama T,
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                                                                                                                                                                                                    Isogai T,
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Human digestive system antigen genomic sequence SEQ ID NO: 4401.

(first entry)

05-NOV-2001 AAK90825;

AAK90825 standard; DNA; 15865 BP

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Human, digestive system antigen, gene therapy; cancer, appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                                                                                                  31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
02-MAR-2000; 2000US-0186350.
16-MAR-2000; 2000US-0189370.
                                                                                                                                                                                                                                                                                                             18-APR-2000; 2000US-0198123.
19-WAY-2000; 2000US-0205515.
07-JUN-2000; 2000US-020467.
28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0215135.
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                                                                                                                                                        WO200155314-A2.
                                                                                                                                Homo sapiens.
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745
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                            Score 504; DB 22; Length 1780;
Pred. No. 4.1e-145;
0; Mismatches 1; Indels 41;
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84.3%; Best Local Similarity 93.0%; Matches 555; Conservative 0

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PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229343.

PR 05-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229345.

PR 06-SEP-2000; 2000US-0229345.

PR 06-SEP-2000; 2000US-0229345.

PR 06-SEP-2000; 2000US-0229343.

PR 06-SEP-2000; 2000US-0229343.

PR 06-SEP-2000; 2000US-0229343.

PR 06-SEP-2000; 2000US-0229343.

PR 14-SEP-2000; 2000US-0221244.

PR 14-SEP-2000; 2000US-0221397.

PR 25-SEP-2000; 2000US-0221398.

PR 25-SEP-2000; 2000US-0221398.

PR 25-SEP-2000; 2000US-0221398.

PR 25-SEP-2000; 2000US-0221397.

PR 25-SEP-2000; 2000US-0221398.

PR 25-SEP-2000; 2000US-022198.

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62 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
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74.7%; Score 447; DB 22; Length 15865;
Best Local Similarity 98.9%; Pred. No. 5.1e-127;
Matches 450; Conservative 0; Mismatches 5; Indels 0;
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17-NOV-2000; 2000US-0249212.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-024924.
17-NOV-2000; 2000US-024924.
17-NOV-2000; 2000US-024924.
17-NOV-2000; 2000US-024926.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-025188.
0S-DEC-2000; 2000US-0251866.
0B-DEC-2000; 2000US-0251866.
0B-DEC-2000; 2000US-0251869.
0B-DEC-2000; 2000US-0251869.
0B-DEC-2000; 2000US-0251869.
0B-DEC-2000; 2000US-0251899.
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GGCTTGCATGGTTAAGCACACACAGAACTGAAGCGCAAAAAGGGTCAGCTGTCTTCATCTAG

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GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAG

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14597 CCCCCATCCATCCTTCCTTCCTTCCTCTCCAACTTGAGTTGTGTCATTCGCACCA 14538

CCCCCATCCATCCCTTCCCTGTTCCCTCCCCAACTTGAGTTGTGTCATTCGCACCA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonuclectide complementary
to the complementary strand of a polynuclectide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonuclectide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 3'-end sequence.
C gequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
characterion and/or diagnosis of the abnormality of the proteins encoded by
the full-length without any specialised methods. AAM133166 to AAM13528 and
AAM13633 to AAM18742 represent human cDNA sequences; AAB92446 to
                                                                       14417 AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG 14358
                                                         421
                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
                                                         CTTTGICCTGGICCGGGICACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K,
, Otsuki 1
                                                                                                                    TICTITIGECATCACCTTCATCCACCTACAGGTAAA 14263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 3986; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi K, S
A, Nagai K,
                                                                                                      TTCTTTTGTCATCACTTCATCCACCTTCTGCCATA
                                                                                                                                                                                                                                                               SEQ ID NO:3986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T, Nishikawa T,
                                                                                                                                                                                         BP.
                                                                                                                                                                                      AAH07151 standard; cDNA; 618
                                                                                                                                                                                                                                                            Human cDNA clone (5'-primer)
                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000JP-0241899
                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Full-length cDNAs
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-2000;
                                                                                                                                                                                                                                      26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1999;
                                                       362
                                                                                                      422
                                                                                                                              14297
                                                                                                                                                                                                              AAH07151;
          302
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                                                                                                                                                                 RESULT 10
AAH07151/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
                       represent oligonucleotides, all of which are used in the exemplification
AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                               TGGNAGGTGGAAGGGCTTGCATGGTTAAGCACACCACAAANTNAAGCGCAAAAAGGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTTCTTCCATTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTCTTGTCTGCTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTC
                                                                                                                                                                                                                                                229 TGGGAGGTGGGAGGCTTGCATGGTTAAGCACCAGAACTGAAGCGCAAAAGGGTCAGC
                                                                                                                                                                                                                                                                                                                                                  TGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGGATGATATCGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGGCAGCTIAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCC
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                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                               ;
0
                                                                                                                                                Length 618;
                                                                                                                                                                                               5; Indels
                                                                                               Sequence 618 BP; 186 A; 135 C; 145 G; 149 T; 3 other;
                                                                                                                                              22;
                                                                                                                                              Score 364.4; DB 22
Pred. No. 3.4e-102;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 3742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAIS97S3/c
ID AAIS97S3 standard; cDNA; 1103 BP.
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2000US-0552317.
2000US-0598042.
                                                                                                                                                60.9%;
                                                                                                                                                                  98.68;
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2000US-0662191
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2000US-0727344
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                                                 the present invention.
                                                                                                                                                                                            Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGATTGTTG 598
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200153312-A1
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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09-JUL-2000;
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WO200229086-A2
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                                                                                                              ABQ58609;
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                                                            RESULT 12
                                                                          ABQ58609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                      Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                 and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 AGGAACCATGTTCCAACACCCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1038 AGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGGGTAAGATACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCCATCCATCCTTCCTTCCCTGTTCCCCT-CCCAACTTGAGTTGTGTCATTCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCCATCCATCCTTCCTTCCCTCCCCCCCAACTTGAGTTGTCTCATTCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCC-TGGGAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGTCCTGGGTGGTGGGTGCTACAGCCACCTAAGGCAAGGAGCCCTTGGGAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 AGGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 ATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 344.4; DB 22; Length 1103;
Pred. No. 6.9e-96;
0; Mismatches 2; Indels 111; Gaps
                          Wang
                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders
                        Ren F, W
Zhang J;
                        Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1103 BP; 303 A; 242 C; 290 G; 268 T; 0 other;
                       Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                  Claim 1; SEQ ID NO 3742; 10078pp; English.
                                                                                                                          such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.1%;
Matches 486; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                         WPI; 2001-442253/47.
(HYSE-) HYSEQ INC
                                                                                       P-PSDB; AAM40597
                                                                                                                                                                                                                                                                                                                                          N.S disorders.
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                       Tang YT,
Wang J, 1
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
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AB056306 to AB060787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78991 to ABB7004 represent proteins encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be used in antisense therapy An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the phenotype of cells in a sample of colon cancer in a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise artibodies, and to screen for peptide analogues and antagonists.
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66. GCTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 ACTGCGATTAAAAAAAAAGCACTTCTGCCAAAGGAACCATGTTCCAACACCGCAAACAAG 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dwivedi P, Molino GA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human colon cancer related nucleotide sequence SEQ ID NO:2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; colon cancer; cancer; tissue profiling; forensic; m
genetic analysis; diagnostic; antisense therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.0%; Score 322.8; DB 24; Length ilarity 97.5%; Pred. No. 1.9e-89; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 361 BP; 91 A; 102 C; 81 G; 82 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carroll E,
                                                                                                                                                                                                                                           ABQ58609 standard; cDNA; 361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2000; 2000US-237271P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2001; 2001WO-US30732
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 796pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burgess C, Astle JH,
Thiaglingam A, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-426115/45.
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les 346; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARB ) BAYER CORP.
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5 256

Gaps

9

Indels

Length 390;

23;

430

ABV13617/c RESULT 13

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489

91

88.

Yamamoto J;

Claim 1; SEQ ID 561; 2537pp + CD ROM; English.

(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.

Sequence 390 BP; 126 A; 74 C; 104 G; 86 T; 0 other;

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GATGCTTCAACCCCCTAAGGCCAGGAGCCCTTGGAAGGTTGGAAGGCTTGCATGGTTTA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTATTATATTAGTTGATGTTGAAATTCAGAAAACAAAATCTCATTCTTGTCTGCTGNAAGAG 549
                                                                                                                                                                              GCACA-CCAGAACTGAAGCGCAAAAGGGTCAGCTG----TCTTCATCTAGAATCTCTGGA 311
                                                                                                                                                                                                                                                                                      GTTCCTTCCAAAAAGCATTCCCCATGATATCGCAGTGCAAGGGCCCTGGCTTTGTCCTG 211
                                                                                                                                                                                                                                                                                                                                                                 Gracedercacreccarcritiricerrecarricaedecaecriaarriterrier 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTGTCTTGTCTGCAAGAG 31
                                                                                                                                                                                                                 GCCCCCCCAGAACTTAAGCGCAAAAGGGTCAACTGTTTTTCATCTTAAAATTTCTGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTG
                                                                                                                                                                                                                                                                                                                                GTCCGGGTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAA-TTTCTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                         431 CATCACTICAT-CCACCTICTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                GATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGA--GGTGGGAGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iikawa T, Hayashi K, Saito K,
Wakamatsu A, Nagai K, Otsuki
                         .7e-70;
38;
                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA clone (5'-primer) SEQ ID NO:561
                         Score 259.8;
Pred. No. 5.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICCCIGIAAICICCCIIGGGCIIGIAC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCCTGTAATCTCCCTTGGGCTTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH03726 standard; cDNA; 856
                         43.4%;
ilarity 87.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
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                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1074617-A2
                         Query Match
Best Local Simi
Matches 341;
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Ishii S,
                                                                                                                                      390
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                                                           270
                                                                                                240
                                                                                                                                    AAGCGCAAAAGGGTCAGC-TGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCA 329
                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, prostate cancer, cytostatic; carcinogen, pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
ACCTAAGGCAAGGAGGTGGGGGGGGTTGCTTAAGCAAGGCACACGAACTG
                                                           ACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAACTG
                                                                                                                                                                                                               383
                                                                                                                                                                                                               TCCCCGATGATATCGCAGTG-CAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACT
                                                                                                                                                                                                                                         TCCCCNATGATATCGCANTGCCAAGGACACTGNCTTTGGCCTGGTCCGGNTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 13608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2258; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monahan JE;
                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                              ABV13617 standard; cDNA; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2001
                                                                                            181
                                                                                                                                  271
                                                         211
                                                                                                                                                                        241
                                                                                                                                                                                                             330
                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                   ABV13617;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence, where the coligonucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, the complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the price of the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the price of the full-length and seasily without any specialised methods AAH13631 to AAH13631 to AAH13631 represent human cDNA sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 ATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCAT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617
                                                                                                                                                                                                                                                                                                                                                                                                                represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTGCCATATCAACACACTCCCTTTCCTATACATCGCCGCCTCATTATTATAGTTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTC-TTTTGTCATCACTTCATCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTTTTGTCATCACTTCATCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgaatrcagaaacanaarcrcarrcrrgrcrgcrgcaagagrrcccrgraarcrccrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; carcinogen; pharmacodyanamic
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 856 BP; 248 A; 183 C; 222 G; 196 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 237.4; DB 22;
Pred. No. 7.1e-63;
----renes 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCTTGTACTGGTGTTAGTCCAGATTGTTG 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCTTGTACTGGTGTTAGTCCAGATTGTTG 586
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.7%;
94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer;
pharmacogenomic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV34731;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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XCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
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The invention relates to an isolated nucleic acid molecule (I) comprising a nuclectide sequence given in Tables 1-9 (BABV0010-ABV62213) of the CC specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate

(d) assessing the efficacy of a therapy for inhibiting prostate cancer

(i) a patient;

(ii) a patient;

(iii) a patient;

(iii) a patient;

(iii) a patient;

(iii) a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463
                                                                                                                                                                                                                                                                                                                                                      comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTCCCTTTCCTATACATCGGCGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 AGTGCAAGGGCCTGGCTTTGTCCTGGTCCGGGTCATCTTTTTTTCCTTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTTGGCAGCTTAA-TTTCTTTTGTCATCACTTCAT-CCACCTTCTGCCATATCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cregregeagerrarrrrrrrrrrrrrrarcacrrcracerccrrcreceararcae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATCTCATTCTTGTCTGCTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTAC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AATCTCATTCTTGTCTGCTGCAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTAC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 202.6; DB 23; Length
Pred. No. 2.3e-52;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 287 BP; 97 A; 55 C; 81 G; 54 T; 0 other;
                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                         Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.9%;
                                    2000US-211314P.
2000US-219007P.
                                                                             2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.9°
Best Local Similarity 97.0°
Matches 227; Conservative
                                                                                                                                                                                             WPI; 2001-662795/76.
                25-MAY-2000;
09-JUN-2000;
                                                                           13-DEC-2000;
                                                           18-JUL-2000
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Search completed: July 12, 2003, 13:44:15 Job time : 164 secs Appli Appli Appli Appli Appli Appli

Sequence

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Sequence 1 Sequence 1 Sequence 1

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Run on:

Sequence:

Searched:

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DB 1; Length 7218;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: 62
STREET: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
             US-09-215-131-3
US-08-22-734-3
US-08-890-853-1
US-09-099-125A-1
US-09-197-008-1
US-09-197-008-1
US-09-197-008-1
US-09-032-476-1
US-09-03-34-1
US-09-023-34-1
US-09-023-34-1
US-09-023-34-1
US-09-023-34-1
US-09-03-34-1
US-09-15-131-1
US-09-215-131-1
                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Foley & Lardner
: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                           22268
22268
222668
222668
222668
33966
2414
2488
74145
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                                                              US-08-232-463-14
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CITY:
STATE:
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 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Sequence 101, App
                                                                                                                            (without alignments)
4168.016 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
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1 ttggaatagttcttgcttta......ggtgttagtccagattgttg
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                                                                                                           ; Search time 44 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-998-003A-96
US-08-453-274B-96
US-08-453-695A-96
US-08-268-161A-96
US-08-453-702A-96
US-09-099-639-96
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PCT-US95-08071-96
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-568-459A-1
US-08-487-826B-1
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US-09-128-155-16
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                                                                                                                                                                                                                                                                                441362 seqs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - nucleic search, using sw model
                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                          July 12, 2003, 13:38:58
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents NA:*
                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                         US-09-914-191-1
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                                                                                                                                                                                                                                    Scoring table:
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35.55

Result ٠ و υU

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Sequence 1, Application US/08568459A

| Pacent No. 5849306
| GENERAL INFORMATION:
| APPLICANT: Sim; Kim L. |
| APPLICANT: Miller, Louis H. |
| APPLICANT: Miller, Louis H. |
| APPLICANT: Wellems, Thomas E. |
| A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 CTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 TICITITGICALCACCITCCACCITCTGCCATALCAACACACACCCTTTCCTATACAT
                                                                                                                                                                                                                                                                          Length 43795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38854 CTTCTTCTTTTTTTTTTTTTTTTTTTTTGAGA 38819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482 CGGCAGCTCATTATATAGTTGATGTTGAATTCAGA 517
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                                                                                                                                                                                                                                                                             6.6%; Score 39.2; DB 3;
                                                                                                                                                                                                                                                                                                      0.048;
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/08/568,459A
07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plasmodium vivax
                                                                                                                                                    TOPOLOGY: linear . MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                      53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,6
                                                            LENGTH: 43795 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4084 base pairs
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         83; Conservative
                                                                                                                              single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 83; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07
                                                                                           TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-568-459A-1/c
                                                                                                                                                                                                                    US-08-742-185-101
                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                     106 AGAGTAAGATACACCCCCCATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGT 165
                                                                                                                                                                                                                    166 TGTGTCATTCGCACCAGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAG 465
                                                                                                                                                                                                                                                                                                                                      226 CCCTGGGAGGTGGGAGGGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 AGCTGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton Darri
   Best Local Similarity 4.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 216; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-0CT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/690,734
FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/310,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1417 YYYYYYYYYYYYYYYYYYGTACCAAATTCTTCTA 1450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-07A2
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101, Application US/08742185
Parent No. 6020476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET: Two ...
CITY: Lexington
STATE: Massachusetts
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GENERAL INFORMATION:
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TITITCCATCACATITITCTTTCAGTITITGCACTTCTGTGGGCAATTCTGACACGTAAT 1557
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Pred. No. 0.15
0; Mismatches
                                                                                                                                                                    1496 ATTTACAAATCCATATAAAATTC 1474
                                                                                                                                 511 ATTCAGAAACAAAATCTCATTC 533
                                                                                                                                                                                                                                                             Sequence 1, Application US/09210288 Patent No. 6392026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium vivax
                                                                                                                                                                                                                                                                                                                     Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
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Best Local Similarity 53.1%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Ma
STREET: 620 Newport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92660
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                                                                                                                                                                                                                                             -09-210-288-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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APPLICANT:
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APPLICANT: milet., Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
APPLICANT: Peterson, Down S.
APPLICANT: AL MILET S.
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                              1616 ritriricaricacaritriricrirricagritrirgeacriricrigigggggaariceacacciaari 1557
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                                                                                                            391 TITITCCTICCATITCTGTTGGCAGCTTAATTICTTTTGTCATCACTTCATCCACCTTCT 450
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                                    Length 4084;
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                                      DB 2;
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Pred. No. 0.15;
0; Mismatches
                                                                         0; Mismatches
                                    Score 35.8;
Pred. No. 0.
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APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                               1496 ATTTACAAATCCATATAAATTC 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Knobbe Martens Olson & STREET: 620 Newport Center Drive CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                             511 ATTCAGAAACAAAATCTCATTC 533
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 ^
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08487826B Patent No. 5993827
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NAME: Israelsen, Ned
REGISTRATION UNDRER: 29,655
REFERENCE/DOCKET NUMBER: NIH12
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 235-8550
INFORMATION FOR SEQ ID NO: 1:
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                                    6.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 4084 base pairs
                   Query Match
Best Local Similarity 53.1.
Local Similarity 53.1.
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Best Local Similarity 53.1<sup>†</sup>
Matches 76; Conservative
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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APPLICANT: Sim, K
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ORGANISM: Pla
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US-08-568-459A-1
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391 TTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCT 450

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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1616 TTTTTCCATCACATTTTTCTTTCAGTTTTTGCACTTCTGTGGGCAATTCTGACACGTAAT 1557
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                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                  STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
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358 CTGGCTTTGTCCTGGTCCGGGTCACTGCCATCTTTTTTCCTTTCCATTTCTGTTGGCAGCT 417
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                                                                                                                                                                                                                                                                                                                               390 TITITICCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTC
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Pred. No. 0.043;
94; Mismatches 120; Indels
                                                                                                                                                                                                                                                 Score 35.6; DB 2; Length 4 Pred. No. 0.048; 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 AATTCAGAAAACAAAATCTCATTCTTGTCTGCTGNAAGAGTTC 552
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                                                                                                                                                                                                                                                                                         0; Mismatches
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LOCATION: (1)...(289)

CTHER INFORMATION: n = A,T,C or G

US-09-007-005-17
 FELECOMMUNICATION INFORMATION:
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Best Local Similarity 50.9%;
Matches 83; Conservative
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Best Local Similarity 7.8%;
Matches 18; Conservative 9
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                                                                                                                   LENGTH: 451 base pairs
                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                     TELEFAX: 206-442-6678
                                                                                                                                nucleic acid
EDNESS: single
                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: Other US-08-943-087-3
                                                                                                                                      TYPE: nucleic
STRANDEDNESS:
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Pred. No. 0.15;
0; Mismatches 67; Indels
                                                                                                                              Parent No. 5198347

APPLICANT: Miller, LOUIS H.;ADAMS, JOHN H.;KASLOW,
DAVIC C.;PANG, XIANGDOUG
TITLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND
PLASMODIUM KNOWLESI DUFFY RECEPTOR
NUMBER OF SEQUENCES: 27
CURRENT APPLICATION DATA:
APPLICATION DATA:
TILING DATE: 20-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: DOS
FastSEQ for Windows Version 2.0
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APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: LUNN, Paul A
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
                                   1496 ATTTACAAATCCATATAAAATTC 1474
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APPLICATION NUMBER: US/08/943,087
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Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZymoGenetics, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.1%;
Matches 76; Conservative
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Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                         SEQ ID NO:5
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Sequence 3, Application US/09177431 Patent No. 6071700
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                        ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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Best Local Similarity 52.5%;
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
    CORRESPONDENCE ADDRESS:
                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                  Fasse, J. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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STREET: ZZL
                                                          Boston
                                                                                                USA
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                                                                            STATE: N
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                                                                                                                                                                                                                                                                                                              NAME:
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478 ACATCGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCATTCTTGT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 TAATITCTTITGTCATCACTICATCCACCTICTGCCATATCAACACAGGCCCTTTCCTAT 477
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                                    114 NYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 NYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCY
                                                                          538 CTGCTGNAAGAGTTCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCC 589
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                                                                                                54 AYTYTYGYTYAYAYYTYGYTYAYAYAYTYAYGYTYAYAYTYTYGYTYTYGYTYCYCY 3
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                                                                                                                                                                                                                                                             APPLICANT: Szostak, Jack W.
APPLICANT: Szostak, Richard W.
APPLICANT: Szostak, Richard W.
APPLICANT: Szostak, Richard W.
APPLICANT: Roberts, Richard W.
TITLE OF INVENTION: ELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: EUSIONS
FILE REPRENCE: 00786/350007
CURRENT APPLICATION NUMBER: 08/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER PLING DATE: 1997-11-06
EARLIER PLING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASISEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HER INFORMATION: Translation template
                                                                                                                                                                                                           Sequence 17, Application US/09244796 Patent No. 6281344
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OTHER INFORMATION: n = A,T,C or G
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Patent No. 5679566
GENERAL INFORMATION:
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APPLICANT: Jacobson, Allan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                         US-09-244-796-17/c
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1855 CAAGATCACCACCATACTCCAAATCAGAGTCGCTGTCTTCTTCTTCATCATCATCAT 1796
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APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MENA DECAY FUNCTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300 FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 95
SOFTWARE: FRSESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.4; DB
Pred. No. 0.68;
0; Mismatches
Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 1, Application US/08375300
Sequence 1, Application US/08375300
Patent No. 5679566
Patent No. 5679566
APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                 1855 CAAGATCACCACATACTCCAAATCAGAGTCGCTGTCTTCTTCTTCTTCATCATCATCAT 1796
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                                                                                                                                                                                                                                                                   Length 2295;
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                                                                                                                                                                                                                                                                                                                      66; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              350 CAAGGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCATC
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Pred. No. 0.96;
0; Mismatches 66;
                                                                                                                                                                                                                                                                   Score 33.4; DB
Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                        0; Mismatches
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   Query Match 5.6%;
Best Local Similarity 52.5%;
Matches 73; Conservative
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Best Local Similarity 52.5%;
Matches 73; Conservative
                                                                                 2295 base pairs
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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EDNESS: single
                                                                                                           nucleic acid
                                                                                                                                                                              MOLECULE TYPE: DNA
PCT-US95-16930-3
                                                                                                                                                             linear
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ZIP: 02110-2804
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                                                                                                        TYPE: nuclei
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                                                                                                                                                             TOPOLOGY:
                                                                                 LENGTH:
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ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
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PRODUCTION IN THE ABSENCE OF
NONSENSE-MEDIATED MRNA DECAY
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STREET: 225 Franklin Street Suite 3100
CITY: Boston
                                                                                                                                                                                          07917/050001
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ATTORNEY/ACENT INFORMATION:
NAME: FASSE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9516930 GENERAL INFORMATION:
                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/955,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT:
NAME: FRASS, J. PETER
REGISCRATION NUMBER: 32,983
REFRENCE/DOCKET NUMBER: 07917
TELECOMMUNICATION INPORMATION:
TELEFAX: 617/542-9806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 TTTCCTATACATCGCCAGC 488
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 040
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 52.5°
Matches 73; Conservative
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TITLE OF INVENTION: PRO
TITLE OF INVENTION: NON
TITLE OF INVENTION: FUN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-09-177-431-3
                                                                                 FILING DATE
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PCT-US95-16930-3/c
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                                       3304 CAAGATCACCACCATACTCCAAATCAGAGTCGCTGTCTTCTTCTTCATCATCATCAT 3245
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410 TGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCC 469
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                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09177431

Patent No. 6071700

GENERAL INFORMATION:
APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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Pred. No. 0.96;
0; Mismatches 66; Indels 0.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
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APPLICATION NUMBER: 08/955,472
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0791
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 225 Franklin Street
CITY: Boston
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SEQUENCE CHARACTERISTICS:
LENGTH: 4080 base pairs
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Best Local Similarity 52.5%;
Matches 73; Conservative
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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US-09-177-431-1/c
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TELEX: 20
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3304 CAAGATCACCACCATACTCCAAATCAGAGTCGCTGTCTTCTTCTTCTTCATCATCATCAT 3245
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Pred. No. 0.96;
0; Mismatches 66; Indels 0
                                    APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF TITLE OF INVENTION: NONSENSE-MEDIATED MRNA DECAY TITLE OF INVENTION FUNCTION NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson STREET: 225 Franklin Street Suite 3100 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                           COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REJERHONE: (617)542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: July 12, 2003, 14:24:25
Job time : 46 secs
Sequence 1, Application PC/TUS9516930 GENERAL INFORMATION:
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Best Local Similarity 52.5'
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4080 base pair
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EDNESS: single
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02110-2804
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Sequence 17, Appl Sequence 26138, A Sequence 9764, Ap

US-10-083-357-80 US-10-177-293-227 US-10-095-407-16 US-10-095-407-17 0 US-09-864-761-26138 0 US-09-864-761-964 US-10-196-864-7248 US-10-196-698-455 US-10-106-698-455 US-10-106-698-455 US-10-284-466A-1 US-09-844-988-8 US-10-233-406-1 US-09-844-988-8

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Sequence 80, Appl Sequence 227, App Sequence 16, Appl

Sequence 7248, Ap Sequence 455, App Sequence 1, Appli Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli

Sequence 8, Appli Sequence 50, Appl Sequence 14, Appl Sequence 2713, Ap

Sequence 82, P Sequence 82, P Sequence 82, P

US-09-844-908-8 US-09-71-161A-50 US-09-796-872-14 US-09-784-877-2713 US-10-138-838-82 US-10-138-918-82 US-10-138-916-82 US-10-138-916-82

10010

Sequence 3, Sequence 61, Sequence 82, Sequence 82,

US-10-270-333-61

ALIGNMENTS

Sequence 1,

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APPLICANT: Wang, Dinkui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhong, Us
APPLICANT: Wang, Zhong, Us
APPLICANT: Dinkui
APPLICANT: 2000-06-20
PRIOR APPLICANT: 2000-01-21
NUMBER: OF SEQ ID NOS: 331
SOFTWARE: DF FL_Genes Version 1.0
SEQ ID NO 171
LENGTH: 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 171, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
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APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Xnou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
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APPLICANT: Chen, Rui-hong
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Sequence 10017, A
Sequence 968, App
Sequence 104, App
Sequence 104, App
Sequence 31778, A
Sequence 31778, A
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Sequence 297, App
Sequence 1, Appli
Sequence 11, Appli
Sequence 8420, Ap
Sequence 10, Appli
Sequence 2118, Ap
Sequence 2218, Ap
Sequence 7559, Ap
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8282.800 Million cell updates/sec
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/ cgn2_6/ptodata/1/pubpna/DS06_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/PCTUB_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/DS07_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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                                                                                                                                                                           July 12, 2003, 13:41:28 ; Search time 114 Seconds
                       GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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ORGANISM: Homo sapiens

; NAME/KEY: CDS ; LOCATION: (42)..(938) US-10-098-841-171

Sequence 194, App

US-09-764-877-2529 US-09-960-352-7651 US-09-925-301-227 US-10-125-540-194

2239

33.6

121

Gaps

181

301

361

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
RIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR PILING DATE: 1999-10-29
RIOR APPLICATION NUMBER: US 60/163,280
PRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver: 3.0
SEQ ID NO 968
LENGTH: 557
                                                                                                                                                                                GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGGCCCTGGGAGGTGGGAG 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1066 TICTTITGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACAT 1007
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                                                                                                                                                                                                                                   AGGAACCATGTTCCAACACCCCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCA
                                                                                                                                                                                                                                                                                                                122 CCCCCATCCATCCCTTCCTTCCCTCCCTCCCACTTGAGTTGTGTCATTCGCACCA
                                                                                                                                                                                                                                                                                                                                       CCCCCATCCATCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCA
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                                                                                                                                                          Length 1512;
                                                                                                                   Indels
                                                                           Score 594.4; DB 9;
Pred. No. 6.2e-177;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 968, Application US/10106698; Publication No. US20030109690A1; GENERAL INFORMATION:
                      or
                                                                             99.4%;
                                                                                                                 Conservative
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-968
; LOCATION: 1512
; OTHER INFORMATION: n
US-10-198-846-10017
                                                                           Query Match
Best Local Similarity
Matches 595; Conserv
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US-10-106-698-968/c
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APPLICANT: Mang, Youghao
APPLICANT: W., Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: PREVENTION: PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-0710
PRIOR PILING DATE: 2002-0710
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                ACCCCCATCCATCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACC
                                                                                                                                                                                                                                                                              1101 ACCCCCATCCATCCTTCCTTCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACC
                                                                                                                                                                                                                                                                                                                                                                       1041 AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGAGGTGGGA
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                                                        Gaps
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LOCATION: 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501,
LOCATION: 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511,
                                                          .;
0
                Length 1231;
                                                        1; Indels
                  Score 597; DB 9; I
Pred. No. 8.3e-178;
0; Mismatches 1;
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Publication No. US20030099974A1
GENERAL INFORMATION:
                99.8%;
                Query Match
Best Local Similarity 99.8
Matches 597; Conservative
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US-10-198-846-10017/c
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Length 750

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132 TCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCAGTGTCCTGGG 191
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                                                                                                                                                                                                                                                                                                           623 MK...DMKS.SR.MHTRMY.BBTRHYGH...B.SNT...BKCCYB.TBA.DRM.K.HR.M 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 .B..RA.RBSDR..RCS.MNA.WNWARYTYCST.C.Y...B..HNCSC.MS.Y.KCS... 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 S.SMMAWS.R.SMC..C.H.SM..MA.NDB.SRK..AGHBY.ARNC..SSHTN.RTBCY. 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 IGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTG 371
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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                                  Query Match 6.4%; Score 38; DB 9; Le
Best Local Similarity 9.0%; Pred. No. 0.18;
Matches 39; Conservative 132; Mismatches 263;
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6.4%; Score 38; DB 9; Le
Best Local Similarity 9.0%; Pred. No. 0.18;
Matches 39; Conservative 132; Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 104, Application US/10184634 Publication No. US20030068684A1 GENERAL INFORMATION:
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Gurney, Austin L.
Pan, James
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Goddard, Audrey
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US-10-184-634-104/c
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LENGTH: 750
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                                                                                                                                                                                                                                                                                                                                                                 CCCCCATCCATCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 AATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGG 183
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                                                                                                                       GGCTTGCATGGTTAAGCACACCAGAACTGAAGCGCAAAAAGGGTCAGCTGTCTTCATCTAG
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CURRENT APPLICATION NUMBER: US/10/184,644

CURRENT FILING DATE: 2002-06-28

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612

SEQ ID NO 104

LENGTH: 750
                                                               Gaps
                                                               .
0
Length 557;
                                                               Indels
Score 541.6; DB 9;
Pred. No. 1.6e-160;
1; Mismatches 0;
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Publication No. US20030044930A1
GENERAL INFORMATION:
   90.6%;
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Watanabe, Colin K.
Wood, William I.
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                                                               Conservative
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CORGANISM: Homo Sapien
US-10-184-644-104
                            Similarity
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Length 750;

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica.*A.
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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SWISSPROT HIT: Q37376, EVALUE 1.40e+00
NT HIT: D13987.1, EVALUE 8.80e-01
EST_HUMAN HIT: AV693827.1, EVALUE 2.00e-12
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION WUMBER: US 09/608,408
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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Pred. No. 0.15;
0; Mismatches
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PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PRIOR DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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; Patent No. US20020048763A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             MAP TO AL139805.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.1%;
Best Local Similarity 65.1%;
Matches 54; Conservative
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OTHER INFORMATION:
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US-09-864-761-15256
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LENGTH: 104
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                                                                                                                                                                                                     504
                                                                                                                                                                                                                                                    312 TGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGCTTTGTCCTG 371
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     H..C..H..TY...K..HNKKY.B..NSMH.H..Y.S.MST..A.NMBTS..SH.SBSRA 624
                                                   192 TGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATG 251
                                                                                                                                                     252 GTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTAGAATCTCTGGA 311
                                                                                  623 MK...DMKS.SR.MHTRMY.BBTRHYGH...B.SNT...BKCCYB.TBA.DRM.K.HR.M
                                                                                                                                                                                      563 .B..RA.RBSDR..RCS.MNA.WNMARYTYCST.C.Y...B..HNCSC.MS.Y.KCS...
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00667
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LING DATE: 2000-05-26
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FILING DATE: 2000-08-03
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Patent No. US20020048763A1
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LOCATION: (3667..(369)

OTHER INFORMATION: n equals a,t,g, or C
NAME/KEY: misc feature
LOCATION: (4197..(419)

OTHER INFORMATION: n equals a,t,g, or C
NAME/KEY: misc feature
LOCATION: (4357..(435)

OTHER INFORMATION: n equals a,t,g, or C
NAME/KEY: misc feature
LOCATION: (4437..(443)

OTHER INFORMATION: n equals a,t,g, or C
NAME/KEY: misc feature
LOCATION: (4497..(449)

OTHER INFORMATION: n equals a,t,g, or C
NAME/KEY: misc feature
LOCATION: (4497..(449)

OTHER INFORMATION: n equals a,t,g, or C
LOCATION: (4527..(452)
                    INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                     or
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THER INFORMATION: n equals a,t,g, or AMAB(KEY: misc feature
OCATION: (469)...(469)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n equals a,t,g, o. NAME/KEY: misc feature LOCATION: (474)...(476) OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (484) OTHER INFORMATION: (484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or
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LOCATION: (552)... (552)

OTHER INFORMATION: n equals a,t,g, or
NAME/KEX: misc feature
LOCATION: (564)... (563)

OTHER INFORMATION: n equals a,t,g, or
NAME/KEX: misc feature
LOCATION: (578)... (578)

OTHER INFORMATION: n equals a,t,g, or
NAME/KEX: misc feature
LOCATION: (581)... (581)
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YTHER INFORMATION: n equals a,t,g,
MMEKEY: misc feature
OCATION: (491)...(491)

YTHER INFORMATION: n equals a,t,g,
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WAME/KEY: misc feature
COGATION: (537)..(537).
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WHER INFORMATION: n equals a,t,g,
AMME/KEY: misc feature
CCATION: (589)..(589)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
TOCATION: (644)..(644)
                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (351).
NAMER INFORMATION: n equals a,t,g,
NAMEX: misc_feature
LOCATION: (366)..(369).
                                                                                      LOCATION: (337)..(337)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCATION: (537)
THER INFORMATION: n equals a,t,g,
WE/KEY: misc_feature
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THER INFORMATION: n equals a,t,g,
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OCATION: (619)..(619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3112, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 TCACTGCCATCTTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 reactrecageatrariaecrectricitricitractriaerrecarreateagri 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: MAP TO AL139805.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.6
US-09-864-761-1525.
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00670
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR PPLICATION NUMBER: US 60/234,687
PRIOR PFLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.1%; Score 36.6; DB 10; Best Local Similarity 65.1%; Pred. No. 0.43; Matches 54; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (252). (252)
CHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (295). (295)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (313)...(315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 CATCCACCTTCTGCCATATCAAC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 CÁTTCACTTTTCAATTATCCAC 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (335)..(335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-106-698-3112
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LENGTH: 734
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Su, Xin-zhaun
Su, Xin-zhaun
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1616 Tritriccarcartritricritricagritritgeacritcrigigggedaritcreacacerari 1557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 TTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCT
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Publication No. US20030092013A1

GENERAL INFORMATION:
APPLICANT: MCCATCHY, Jeanette
APPLICANT: Ableson, Allen
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
CURRENT APPLICATION UNMBER: US/10/020,141

CURRENT APPLICATION UNMBER: US/10/111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Indels
                                                                                                                                                                    ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35.8; DE
Pred. No. 2.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/210,288
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Plasmodium vivax
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1496 ATTTACAAATCCATATAAAATTC 1474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%;
Local Similarity 53.1%;
les 76; Conservative
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-020-141-11/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1789 GCAAAAAAAAATGTCAAGAGTATTTATTACCGATAAATGAACATTTAACTAGCCTTTT 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 CTGCCATCTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTTTGTCATCACTTCAT 441
                                                                                                                                                                                                                          403 TITICIGITIGGCAGCITAATITICITITIGICATCACCITICATCCACCTICIGCCATAICAACA 462
                                                                                                                                                                                                                                                                           388 TTTTTTTTGAAAAATTTTTTTTTTTTTTTTAAAAAGCCCCTTTANTTTTTTTTAAAT 447
                                                                                                                                                                                                                                                                                                                           463 CAGTCCCTTTCCTATACATCGGCAGCTCATTATTATTAGTTGATGTTGAATTCAGAAACA 522
                                                                                                                                                                                                                                                                                                                                                                          448 ANGCNTTTTTTAAAATTGGNCCCCNNNTTTTTTANTTTAAANTTTTTAAAAAAAA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 CCACCTTCTGCCATATCAACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTAGT
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; OTHER INFORMATION: Incyte ID No. US20030119009A1 1292280CB1
US-10-084-817-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                         78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SLEAT Stuart
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Sharon E. Plon
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
FURBENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73;
                                                                                                                      Score 36.2; DB 9;
Pred. No. 0.65;
0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1849 regraregraagagargreaaargrearrer 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 AAATTTTAATTGTTTTTTNNAAAAATTTNCC 539
                                                                                                                                                                                                                                                                                                                                                                                                                          523 AAATCTCATTCTTGTCTGCTGNAAGAGTTCCC 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guery Match
6.1%; Score 36.2; DE
Best Local Similarity 52.3%; Pred. No. 1.2;
Matches 80; Conservative 0; Mismatches
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       CTHER INFORMATION: n equals a, E, g, or US-10-106-698-3112
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Publication No. US20030119009A1
GENERAL INFORMATION:
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Patent No. US20020169305A1
GENERAL INFORMATION:
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Chitnis, Chetan
Miller, Louis H.
                                                                                                                      Query Match
Best Local Similarity 48.7%;
Matches 74; Conservative
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LENGTH: 201
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331 CCCCGATGATATCGCAGTGCAAGGCACTGGCTTTGTCCTGGTCCGGGTCACTGCCATCT 390
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                     Length 432;
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                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 111;
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63; Mismatches 258;
                                                                                                                                                                                                                                                                                                                   5.9%; Score 35.4; DB 9; 43.1%; Pred. No. 0.85;
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CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
    PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 10, Application US/10123155; Publication No. US20030068794A1; GENERAL INFORMATION:
                                                                                                                                                                                                                         LOCATION: (1) ... (432)
COTHER INFORMATION: n = A,T,C or G
US-09-918-995-8420
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.1
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DeForge, Laura
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                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                  NAME/KEY: misc_feature
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Best Local Similarity
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Publication No. US20030096248A1
GENERAL INFORMATION:
APPLICANT: MCCATTHY, Jeanette
APPLICANT: Daley, George
APPLICANT: Bolk, Stacey
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-003
CURRENT APPLICATION NUMBER: US/10/017,721
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/317,033
PRIOR PELING DATE: 2001-10-17
PRIOR FILING DATE: 2001-10-17
PRIOR FILING DATE: 2001-10-17
PRIOR FILING DATE: 2001-10-17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 185695
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-75
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                         Pred. No. 25;
0; Mismatches
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                                                                                                                                                                                                                                                                   6.0%; Score 35.8;
59.2%; Pred. No. 25
PRIOR APPLICATION NUMBER: US 60/313,097
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/327,485
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                       Best Local Similarity 59.2
Matches 61; Conservative
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Best Local Similarity 59.2
Matches 61; Conservative
                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-10-017-721-1
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-10-017-721-1/c
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US-10-020-141-11
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                              445 CCSDYYCYSYSYSYSYSYSYSYSYSYTDYCSYRRCCCYYSYSSSYSSSAST 386
116 ACACCACCCCCATCCATCCCTTCCCTGTTCCCTCCCAACTTGAGTTGTGTCATTC 175
                            505 SYS.S.SWSSSYSYSSSDDY, CYCCYYRYHCSDSYSYSYYY, CRCCYYT, SYSRYDCHYSC 446
                                                                                                                                                                               236 TGGGAGGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTC 295
                                                                                                                                                                                                                                                                          296 ATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGG 355
                                                                                                                                                                                                                                                                                                    385 SSSSSSSYYYTSTNYC.T.CC...T..MCAABCSTTTTTTTTTT..HSCC.SA..A, 326
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Pred. No. 2.4;
0; Mismatches 38;
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
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PRIOR SPELICATION INVIBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2718
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Best Local Similarity 60.4%;
Matches 58; Conservative
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AV718160 AV718160
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 560)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Copyright (c) 1993 - 2003
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400

Score

Result No.

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cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com"

a 224 c 178 g 252 t 14 others
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Frul-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 7.9e-127;
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                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
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Pred. No. 3.7e-142;
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Best Local Similarity 99.8%;
Matches 555; Conservative
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/clone="InAGE31010614"
/clone="InAGE31010617"
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1 (bases 1 to 479)

NIH-MGC http://mgc.nci.nih.gov/,
NIH-MGC http://mgc.nci.nih.gov/,
Other_ESTs: bb55g04.y1

Other_ESTs: bb55g04.y1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rdmail.nih.gov
Tissue Procurement: ATCC
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JUCTALLY...

JUCTALLY...

JORGANISM="Homo sapiens"

/dD xref="taxon:9606"

/clone="IMAGE:5013768"

/clone="IMAGE:5013768"

/tissue_type="epidermoid carcinoma, cell line"

/tab_host="DH10B (phage-resistant)"

/note="Organ: salivary gland; Vector: porB7; Site_1: Xho1;

Site_2: EcoR1; cDNA made by oligo-dT priming.

Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M: Rubin

(University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                        B1084544 881 bp mRNA linear EST 20-JUN-2001
602669101T1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013768 3',
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1 (bases 1 to 881)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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TCCCTTGGGCTTGTACTGGTGTTAGTCCAGATTGTTG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for thGG, ArGG, ArGG, GGGCC, GGAAG, TAGC, TAAGC, ArGG, ARGG, ATCAC. For additional information, contact: Bento Soares, bento-soares@wiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 01-JUN-2000
mRNA sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.

(bases 1 to 577)

(bases 1 to 577)

(based, A. I., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 CCCCCATCCATCCCTTCCTTCCCTTCCCTCCCAACTTGAGTTGTGTCATTCGCACCA
                                                                                                                                                                                                                                                                                                                                                                                                     CCCCCATCCATCCCTTCCCTGTTCCCCTCCCCAACTTGAGTTGTGTCATTCGCACCA
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Corract: John Quackenbush
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW954708 577 bp mRNA linear EST366778 MAGE resequences, MAGC Homo sapiens CDNA,
                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                       74.6%; Score 446; DB 14; I
100.0%; Pred. No. 3.9e-112;
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                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0%; Pred. No. 3.9 Matches 446; Conservative 0; Mismatches
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TAG TISSUE-Fetal thymus
TAG SEQ=AACG"
121 c 95 g 14
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MMAGE: 3104658 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Thissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                          365
                         66 AAGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACC 125
                                                                           ACCCCATCCATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACC 180
                                                                                                                                                       240
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                                                                                                                                                                                                                                                                                                                                                                                                     126 ACCCCCATCCATCCTTCCTTCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACC 185
                                                                                                                                                                                          186 AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGA 245
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. (Loase) 1 to 466)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                           306 GAATCICTGGATGTICCTICCTGGAAAGCATCCCCGATGATATCGCAGTGCAAGGCACTG
                                                                                                                                                       AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAAGGCAAGGAGCCCTGGGAGGTGGGA
                                                                                                                                                                                                                             GGGCTTGCATGGTTAAGCACACACACAAAGCGCAAAAGGGTCAGCTGTCTTCATCTA
                                                                                                                                                                                                                                                                                                     GAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTG
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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COMMENT

us-09-914-191-1.rst

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/db xref="Homo sapiens"
/db xref="taxon:9506"
/clone=IngAgE:1457126"
/clone inb="NoT CAPE_Kid3"
/clone inb="NoT CAPE_Kid3"
/lab host="DH10B" CAPE_Kid3"
/lab host="DH10B" xdney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia) digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "120 t
cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NII-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA308526 427 bp mRNA linear EST 18-APR-1997 EST179347 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTGGC 362
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Pred. No. 2.5e-109;
0; Mismatches 2;
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Matches 437; Conservative
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1 (bases 1 to 439)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                    577;
                                                                                                                                                                                                                                                                                Score 440.8; DB 10; Length
Pred. No. 1.1e-110;
0; Mismatches 16; Indels
                                                                                                                                                                                                                              111 others
 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                    /db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGC"
/note="Vector: pBluescriptSKm"
102 c 123 g 9 t 111 a
                                                                                                                                 1. .577
/organism="Homo sapiens"
                                                                                              Seq primer: Reverse.
Location/Qualifiers
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                                                        Email: johnq@tigr.org
Plate: 67
                                                                                                                                                                                                                                                                                73.78;
96.28;
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stops: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA877204 1.00 432 bp mRNA linear EST 25-MAR-1998 0b09907.sl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1323228 3',
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GNAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTT 128
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                                                                                 531
                                                                                                                                                                                       TCTTGTCTGCTGNAAGAGTTCCCCTGTAATCTCCCTTGGGCTTGTACTGGTGTTAGTCCAG 591
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                                                                                                              TCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGAATTCAGAAAACAAAATCTCAT
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/clone="IMAGE:1323228"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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Best Local Similarity 97.4%;
Matches 407; Conservative
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                                                                      Adams, M.D. Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.D., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G. Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedhlom, E. Hinkle, P.S. Jr., Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Rycker, S.E., Soctt, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.M., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J.; Fannon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 GCAGCTTAATTTCTTTTGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTT 471
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="HCC cell line (matastasis to liver in mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="KM12C(HCC)metastasis into mouse (liver)"
/cell_line="KM12C(HCC)metastasis into mouse (liver)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCCGATGATACGCAGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 ATTCGCACCAGTGNCCTGGGTAGGATGCTACAGCCACCTAAGGNAAGAGCCCTGG
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The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 421; DB 9; Length 42
Pred. No. 3e-105;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="ATCC (inhost):112370"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Contact: Kerlavage, AR
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ilarity 98.8%;
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AU134061 618 bp mRNA linear EST 01-AUG-2002 AU134061 OVARCI Homo sapiens cDNA clone OVARC1001188 5', mRNA
                                                                                                                                                                                                                                                                                         61 AAGGAACCATGTTCCAACACGCAAAAGGTGTTCTGCTTAAACAGAGTAAGATACACC 120
                                                                                                                                                                                                                                                                                                                                                                                                   121 ACCCCCATCCATCCTTCCTTCCTTCCTCCTCCCCAACTTGAGTTGTGTCATTCGCACC 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 618)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pax: 81-438-52-3986
Bmail: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute
M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
                                                                                                                                                                                                                                                                                                                     AAGGAACCATGTTCCAACAAACAAAGGTGTTCTGCTTAAACAAGGTAAGATACACC
                                                                                                                                                                                                                                          1 Trggaaragrictrgctrrataraaarragracrgcgartaaaaaaaaggactrcrgcca
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
                                                                                                                          DB 14;
                                                                                                                                                                   0; Mismatches
                                                                                                                          Score 370.8;
Pred. No. 2.1
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/db_xref="taxon:9606"
/clone="OVARC1001188"
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AU134061.1 GI:10994600
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Unpublished (2000)
                                                                                                                      62.0%;
99.5%;
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zd93f03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:357053 3', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 374)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashU-Merck EST Project

Unpublished (1995)
                                                                                                                                             GTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGT-GGGA 240
76 AGGAACCATGTTCCAACACGCGCAAACAAGGTGTTTCTGCTTAAACAGAGTAAGATACACCA 135
                                                              181
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                                                                                                                                                                                                                                                                                                               GAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGATGATATCGCAGTGCAAGGGCACTG 360
                                                                                                                                                                                                                                                                                                                                           315 GAATCTCTGGATGTTCCTTCCAGAAGCATCCCCGATGATATCGCAGTGCAAGGCACTG 374
                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final Percentage Savailable royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 466 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 333.
Location/Qualifiers
                                                                                                                                                                            196 GTGTCCTGGGTGGTAGGGATGCTACAGCCACTAAGGCAAGGAGCCCTGGGAGGTGGGGA
                                                              CCCCCATCCATCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACCA
                                                                                      136 CCCCCATCCATCCTTCCTTCCCTGTTCCCTCCCAACTTGAGTTGTGTCATTCGCACCA
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sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:1273597"
/db_xref="taxon:9606"
/clone="IMAGE:357053"
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W93044.1 GI:1422215
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AL530910 I GI:12794403
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                                                                                                                                                       288
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                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li, Chases I to 929)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                TGTCTTCATCTAGAATCTCTGGATGTTCCTTCCAGAAAGCATCCCCGGATGATATCGCAGT
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                                                                                                                                                                                   618 TGGNAGGTGGAAGGCCTTGCATGCTTAAGCACCACAGAANTNAAGCGCAAAAGGGTCAGC
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Genoscope - Centre National de Sequencage
BP 191 91006 FYRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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0
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                                               3 others
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              /tissue_type="ovary, tumor tissue"
/note="Vector: pME18SFL3"
135 c 145 g 149 t 3
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/lab_host="DH108"
                                                                                       Ouery Match 60.9%; Score 364.4; DB 9; Best Local Similarity 98.6%; Pred. No. 1.2e-89; Matches 365; Conservative 0; Mismatches 5;
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/clone="CS0DD003XJ17"
clone lib="OVARC1"
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 357).

1. (bases 1 to 357).

1. Nulliar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

1. Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
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by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Cer
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
206 c 239 g 220 t l others
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This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 466 Std Brror: 0.00
Seg primer: mob_REGA+ET
High quality sequence stops:
Location/qualifiers
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Pred. No. 1.5e-85;
1; Mismatches 1
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99.2%;
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Best Local Similarity 99.2
Matches 360; Conservative
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source

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/db_xref="taxon:9606"
                                                                                                            Location/Qualifiers
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91 c 77 q
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 365)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAAAGGANCCATGTTCCAACACCGCAAACNAGGTGTTCTGCTTAAACAGAGTAAGATAC
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                                                                                                                                                                                                                                                                                                                            2 others
                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
1. 357

/organism="Homo sapiens"

/db_xref="GDB:1273597"

/db_xref="taxon:9606"

/clone="IWAGE:357053"

/clone="lib="Soares_fetal_heart_NbHH19W"

/sex="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
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Matches 347; Conservative
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Unpublished (1997)
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Query Match

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BASE COUNT

ORIGIN

51

LOCUS DEFINITION

RESULT 14 BQ776022

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

AUTHORS TITLE REFERENCE

JOURNAL COMMENT

/dev stage="Adult"
// lab_host="DH10B (Life Technologies)"
// lab_host="DH10B (Life Technologies)"
// lab_host="DH10B (Life Technologies)"
// note="Organ: Bone; Vector: pTT3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I: Site 2: Not I;
NCI_CGAP_FH0 is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, dispeted with Not I, and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT):B tail. The sequence tag for this library is AGATUCGGC. The cell line was provided by Dr CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYAAYES 1044 bp mRNA linear EST 02-APR-2002 AGENCOURT 7046660 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:8806655 BQ073764 ö 240 77 AAGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACC 136 196 61 AAGGAACCATGTTCCAACACCGCAAACAAGGTGTTCTGCTTAAACAGAGTAAGATACACC 120 121 ACCCCCATCCATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGTCATTCGCACC 180 241 GGGCTTGCATGGTTAAGCACAGAACTGAAGCGCAAAAGGGGTCAGCTGTCTTCATCTA 300 257 GGGCTTGCATGGTTAAGCACACAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCATCTA 316 9/ TAG_LIB=UI-H-FH0 TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1 Chondrosarcoma 137 ACCCCCATCCATCCCTTCCTTCCCTGTTCCCAACTTGAGTTGTGTCATTCGCACC 181 AGTGTCCTGGGTGGTAGGGATGCTACAGCCACCTAAGGCAAGGAGCCCTGGGAGGTGGGA Gaps ; 0 Score 344.4; DB 14; Length 365; Pred. No. 3.9e-84; /clone="UI-H-FHO-bck-1-14-0-UI" /clone lib="NCI CGAP FHO" /tissue_type="Human Chondrosarcoma Cell Line" 1; Indels James Martin from University of Iowa

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220 AAGGAGCCCTGGGAGGTGGAGGCTT-GCATGGTTAAGCACA-CCAGAACTGAAGCGCA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACACACAGTCCCTTTCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGAATTCAGA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2047 row: m column: 24
High quality sequence stop: 715.
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                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          NIH-MGC http://mgr.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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 BQ073764.1 GI:19902810
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Best Local Similarity 98.2
Matches 374; Conservative
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AUTHORS
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